

50	55	60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp		
55	70	80
Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala		
	85	90
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly		
	100	105
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val		
	115	120
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala		
130	135	140

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly		
1	5	10
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr		
	20	30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly		
	35	40
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Glu Tyr Asp		
	50	55
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe		
	65	70
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp		
	85	90
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr		
	100	105
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg		
	115	120
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp		
130	135	140

(3) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65           70           75
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 80           85           90
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100          105          110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115          120          125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130          135          140
Gly Cys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145          150          155          160
Lys Asn Pro

```

(2) INFORMATION FOR SEQ ID NO:279:

(A) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(E) MOLECULE TYPE: protein

(F) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1           5           10           15
Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val
 20           25           30
Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35           40           45
Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50           55           60
Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65           70           75
Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 80           85           90
Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100          105          110
Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115          120          125
Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130          135          140
Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145          150          155          160

```

```

Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
      165      170      175
Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
      180      185      190
Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
      195      200      205
Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
      210      215      220
Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
      225      230      235      240

```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
  1           5           10           15
Leu Asn Ala Leu Ala Tyr
      20

```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
  1           5           10           15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
      20      25      30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
      35      40      45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
      50      55      60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
      65      70      75      80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
      85      90      95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
      100     105     110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly

```

115	120	125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln		
130	135	140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro		
145	150	155
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu		
165	170	

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala		
1	5	10
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Ala Thr		15
	20	25
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr		30
	35	40
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg		45
50	55	60

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp		
1	5	10
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr		15
	20	25
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu		30
	35	40
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala		45
	50	55
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile		60
	65	70
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu		75
	80	85
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln		90
	95	100
	105	110

Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Pro Ile Glu
 115 120 125
 Arg Gly Ser Gln Phe
 130

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1 5 10 15
 Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
 20 25 30
 Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
 35 40 45
 Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50 55 60

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1 5 10 15
 Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
 20 25 30
 Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
 35 40 45
 Ala Arg Ser Gly Arg His Gly Arg Arg Gly Tyr Arg Arg Trp Ala Asp
 50 55 60
 Arg Gln Arg Arg Gly Arg Arg Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
 20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
 35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60
Pro Ile Pro Val Arg Ala Ala His His Glu
 65           70

```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```

TGGCAGGTAA TACCGTGGAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG      60
CGAACCGTTA TTGACCGCCC GGAGGCCACT CGCTGCGCAC CAAGTGGTGA CTCAGCCGGT      120
TTTCACGGCA ACGAACGGCG GACACACTAC TTGACATTCG ACGAGCAGGC CCGG      174

```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```

TGGCAAAAGG GGTGACGTTT CGTGGGTGG CGCTAGAGAG TTGTGCGAC TTTCCGCTGA      60
CGGTGGCGGG GCACCGCAGC ACTGGTGAGC TCAGCTGGCT AGTGGAGGTT CTCGACGGTG      120
CGCTGGCGAC GATGGCGCCC GAAAGCTTGG CGAGGCGGGT GCTGGCTGTT TTACAGCGCT      180
TGGTCAGGCG GTGGGATCGG CGGCTGCGCG ACCTGACAT TCTGCTGGAC GCGGAGCAGC      240
ATCGACAGCG ACCGGCGCTG CGGGATGTGA GACGCTGGCG ACCCGCGTGG CATACCGGGT      300
TCGCTAAAT CGCTGCGGCA CAGCTGACT CGGTGGCGGT CAGTGGGCGG GATGGTCAGC      360
TGAGTACCG GGAAGTGGAT GCATTGGCG ACCGGCTGGC CACT      404

```

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His
 1           5           10           15
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu
 20           25           30
Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35           40           45
Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50           55           60
Asp Arg Pro Leu Arg Asp Val Asp His Leu Leu Asp Gly Glu His Asp
 65           70           75           80
Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85           90           95
His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
100           105           110
Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
115           120           125
Ala Asp Arg Leu Ala Thr
130

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

GCTTCGACGG CTACGASTAC CTGTTCTGCG TGGGTTGTGC GGGCGGCTAC GAGGACAAGG      50
CGAAGAAGAC CACCAAGGCC GTGCGCGGAG TGTTCGCCCT CCGCGGGGTT AARTACTTGG      120
TGCTGGGCGC TGGGGAACCC TGCACCGGCS ACTCGGCGCG CGGCTCGGCG AACGAGTTCC      180
TCTTCACGCA GCTGGCACA CAGGCGCTCC AGACCTTCCA CGGTTGTGTC GAGGGGTGTG      240
AGACCGTCGA CGCAAGATC GTTGTCACCT GCGCGCACTG CTTCACACCC ATCGGCAGGG      300
AATATCGGCA CTTGGGCGCC AACTACACCC TGCTGCACCA CACCGAGCTG CTCGAATCGGT      360
TGGTGCGCGA CAGAGGGCTG GTGCTGTGCA CTGCGTTTC TCAGGACATC ACCTACCAGC      420
ACCGTGCTCA GCTGGGTGGG CACACAAAGG TGTACGAGGC ACCACGGGAG CTGATCGGTC      480
CCGCGGGGGC CACTGAGCC GAGATGCGCG GCCATGCCGA CGGCAG      526

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTCGCCGCCG	TGATCTGGCC	GGCGAACTTC	GTCAGTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCGCA	TGCCCATGAT	CACCGCACCG	GCGACCTAGCA	CCGCGGCCAT	CCCGGTGGAA	120
TAGACCAACC	CCCGGGTGA	TGCGGGAAGC	TGGAGGCAAA	GAAGACGCG	CCCGACAATG	180
CCGAGGACCA	TGCGCAACCG	ACCCATCCGA	GGGGTAGGCG	TGACGTGCAC	ATCTCGCTCC	240
CGCGGGTAGG	CGACGGCTCC	CAGCGCACTG	GCGAGCATCC	GCACCGGACC	GGTGGCAAAA	300
TAGGTGATGA	TGCGCCGGGT	CAGCCCGACC	AGCGCAAGCT	CACCGAGCGG	GACATCCGCG	360
CCGCGATAGG	ACAGGGCGAG	CAAGCCACCG	GCAACCGCGG	CCACATCGCT	GGACACCTCG	420
AGACCGTACT	GCACCAAGCT	GAAGAGCTGA	ACACTCGCCG	AACGTGCAAC	AGCTCGGAAC	480
AAATTGG						487

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGAAGCGCT	AGAATATGAG	CCGGGGGCAAC	CCGCGCATTTA	CGAGCTTGAG	TTCGGGGGCG	60
CTCAGCTCTC	GTCTGCGGAC	GGCGCTGGTC	CGGTGTTGGT	GCAGCGTTTG	GAAGGTTTCT	120
CGGAGCGCGG	CGATGCGATC	CGGCTGGGCG	CCGCGCACCT	CAAGCGGGCG	CTGGACACAG	180
AGCTGGTGGG	GTCTTTGCGG	ATCGATGAAC	TACTGGACTA	CGGTCGGCGG	CGGCGATTAA	240
TGACTTTCAA	GACCGATCAT	TTCCACCACT	CGGATGATCC	TGAGCTAAGC	CTGTATGCGG	300
TGGCGGACAG	CATCGGACCC	CCATTTCGCG	TGCTGGGGGG	TTTGAGGCGG	GACCTGAAGT	360
GGGAGCGGTT	CATCACCGCC	TGCGGATTGC	TGGCGGAGCG	CGTGGGTGTA	CGGCGAAGCC	420
ATCGGCTGCT	GCACCGTCCC	GATGGCGGTT	CGGCAACAGC	GACCGATCAC	GATGACCGCT	480
CATTCCACAA	ACCGGGAGCT	ATCTCCGATT	TTCACACGTT	CGATCTCC		528

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCAGGCGCGT	CAAGGACCGG	GTGCGCGGCT	TGCTCTGGGT	GCAGCCGAGG	CCGGCGTTGC	60
CGCGCGTTGC	CGCGTTGCGG	CGGATACCGG	GGTTCTCTAC	GGTGCAGCGG	CCGGGAGACA	120
TGCGCTGGCT	GTCTAGGCGG	TCTTGGGCGG	CGCGCGCGTC	ACCGGCTTTC	CGGCGATCGG	180


```

CCCCCTTCCC GCCCCTGGTG GGGGTGGCGG CCTGCTTAC GTATTGTTC ACCGCCCCGG 240
CCCTTGAACC TTTCGCGGTG TCGATCGCGG CTTCGATGGA TCGCCGACC ACGACGTGCG 300
AAGCCTCGCC TCGCCCGGCA GCGCGCCAAC TGTGTGCGG CTCTGCGAT TTGGCCCGCG 360
CGGACGAGAT GATGGCGACC ACCGAGCGCT GCGCCCTCTT GCGCGCGGC AGCGCGGTT 420
CGCGTCAGG GATACGCGA CGGTGCGCGG CGCTTCGGA GATTTCAGG CTGCGTTGCA 480
CGAGATCGAG CAGCGGTGTG CCGAGGAGCT GGGTTAGCCC GTTGGCGCGG CGCTTGTAGC 540
GCGGAGCGCA ATATCGGTGC CCACTCGACC CAACCGGACG TCCATAGCG ACACCATTCG 600
CGGTGATGTC

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
  1          5          10          15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
  20          25          30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
  35          40          45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
  50          55          60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
  65          70          75          80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
  85          90          95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
  100         105         110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
  115         120         125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
  130         135         140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
  145         150         155         160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys
100          105          110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
115          120          125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
130          135          140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Gln Gln
145          150          155          160
Leu

```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu
1           5           10           15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
20           25           30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
35           40           45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
50           55           60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
65           70           75           80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
85           90           95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Ala
100          105          110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
115          120          125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
130          135          140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Arg Ser

```

145	150	155	160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu			
165	170	175	

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Lys	Pro	Val	Lys	Glu	Pro	Val	Pro	Ala	Leu	Pro	Pro	Val	Pro	Pro	Thr
1			5					10				15			
Pro	Ala	Leu	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Val	Pro	Gly	Phe	Pro
20			25					30							
Thr	Val	Pro	Pro	Pro	Gly	Ser	Met	Ala	Pro	Leu	Phe	Arg	Pro	Phe	Ser
35			40					45							
Pro	Ala	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Pro	Ser	Pro	Pro	Leu	Pro	Pro
50			55					60							
Leu	Val	Gly	Val	Ala	Ala	Trp	Leu	Thr	Tyr	Cys	Ser	Thr	Gly	Pro	Ala
65			70					75					80		
Leu	Asp	Pro	Leu	Ala	Val	Ser	Ile	Ala	Ala	Ser	Met	Asp	Pro	Pro	Thr
85			90					95							
Thr	Thr	Cys	Glu	Ala	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Leu	Cys	Arg	
100			105					110							
Gly	Ser	Cys	Asp	Leu	Ala	Pro	Ala	Asp	Glu	Met	Met	Gly	Thr	Thr	Gly
115			120					125							
Ala	Cys	Gly	Arg	Leu	Gly	Gln	Ala	Ser	Ala	Gly	Ser	Arg	Ser	Arg	His
130			135					140							
Thr	Arg	Arg	Cys	Ala	Ala	Ser	Glu	Ile	Cys	Arg	Leu	Arg	Cys	Thr	
145			150					155					160		
Arg	Ser	Ser	Ser	Gly	Val	Pro	Arg	Asp	Trp	Val	Ser	Pro	Leu	Ala	Pro
165			170					175							
Pro	Leu														

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

AATTGGGCAC	GATCAGCACC	AACACCGGCT	TCTTCAACTC	CGGCGACGTC	AATACCGGTA	50
TGGGCAACAC	CGGCGAGCTC	AACACCGGCA	GCTTCAATCC	CGGCGATTCG	AACACCGGGG	100

ATTTCACCC	ANGCAGCTAC	CACACGCGGA	CTCGGAACAT	CCGGCGATT	TACACCGCC	180
CCTTCATCTC	CGGCAGCTAC	AGCAACCGGT	CTTGCGGAGT	GGAAATTATC	AGGGCTCAT	240
GGMTGCAACC	GGCCTTTCGA	ATCCCTCGK	CCAATTCAAC	TCCTCAGCAA	GCTTCGCGCC	300
GCACCTCAGC	CGCGGTGAAT	GATTGAGTTT	AACCGCTNAN	CAATAACTAG	CATTAACCGCT	360
TCGGCGCTCT	AAACGGCTCT	TGAAGGCTTT	TTTGCTGAAA	GGANGAAGTA	TATCCGAGTA	420
ACTGGCGTAN	TACGAAAGGC	GGCAGCGATC	GCTTTCGCAA	CAGTTGCGCA	CGKGAATGCG	480
AATGAGACCC	CTCTTTACCG	GSCATTAACN	CGGGGGTGTN	GGKGTACCC	CCAGCTNACC	540
GCTACCTTGC	CANNSGCTN	AGCCCTCTTT	TGCTTTCTTC	CTTCCTCTCT	CGMCTTGCGC	600
GGTTCGCTTC	AGCTCTAAAT	CGGGGNNCCG	TTTGGGTTTC	CAATTATTGC	TTACNCGCGC	660
CCACGCCAAA	AAATNATNG	GCTTAATGTC	CGTTMTGGG	CNTCCGCGTA	WTNANNGTTT	720
TCGCCCTTNA	CTTTGCTTCC	CTTCCTTATN	NTGAMNCTNT	TTCCACYGGA	AAAMNCTCCA	780
CGNTTYSSES	TTTCCTTTGA	WTNATMEGGR	AATTSCRAAT	CGGCTTCKG	TTMANNTTAA	840
CTTACTTCNA	ATTTCGCGM	TTTNNMATR	TTNSMCKCGM	KNCTCCNKA	SSGNTTTCCT	900
CCCCCTTSS	GKTYCCGCM	G				921

(2) INFORMATION FOR SEQ ID NO:299:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:299:

AATTCCGCCAC	GAGATANGGG	CGCACCGGGG	TCGCCAGCCG	CGGGGACCBT	CGCCAGCACC	60
ACCGGGGTCA	ACAGCACCCAC	GCTGGCTGTC	ANGCAGACCG	CCGCGGTGAT	GGGGGCCBAG	120
ACGGCRAACA	CCTGCGGTAG	CAGTCCGTGC	GACTCCCGCG	TCGCTCGAAC	CATGGCCCGC	180
CGGGCTGCTT	CGAACANGCC	TTGCTCTGTC	ACAGCTTAGC	CAGCAGCCAA	ACCCGACCCA	240
GAACCCCAAC	CGCCCGCCGC	TCGGGNAACC	TGCGGCTATG	KCTGCTGGGG	CGANATCCGC	300
CGATGCGTNA	CAGATGAGCC	CCTGCCCGAA	CGCCGCGCTT	GCTTCGGGGC	AGCCGCTTGG	360
CGCGGGCAAC	CGCGAACCCA	HGAACCGGGC	AAGCAGTATC	ANGCAGACAG	CAATTCTCAA	420
CGGCTAAACG	CTTCAGATCC	AGGGATCTCG	CGGGCCACAC	CGCTCGGTC	TGCAGGCGGA	480
CGCCCTGCTN	GGCGGNCAC	TCCTCAAGAA	TCGNGATCNA	CAGKCTAGGT	CTTCGCGCGA	540
TATSSAAGGN	CCCAACCGNT	TTAAAGCGGC	GAAGAAASTC	TCCTANTGGA	TAAATCAGC	600
CGGGGANCCT	CGCGTGGCM	HTCTYCGGKC	ATTNTTCAAC	GGGTTCNAGC	CGCGGTGCGC	660
CGCACTCTAC	CAAACTTAAG	KTNGGGGNTY	CGGGCGGCTA	ACCGGCTNTK	NGCCCTTAA	720
AAACCGCGNC	YTTCTTGAT	TAMMACCGGN	CGCCGATGCG	CGGCTGCTCC	CANGTCTAAC	780
AMCCYCTESS	MNGGSKTGGG	GAACGCTTCC	CGNCGGCTTC	NTKGTSTCYT	ARMCCCGCGC	840
AAACCGGKYG	GGKTGGCTN	MASSAMNCCG	CMNGYTYCTT	TAAAGGCTAN	KTRAANGKYT	900
CCTTGGGAAN	CTTNCATATC	GAAATYCTC	CTYMMGSSCN	CTTKCWRTYN	NNNGGAGACC	960
AMWNTYCCNC	GWTTTCANTCG	GTCGCCASMN	AAACKECTTY	TTTTCGSSC	STCCMGGNC	1020
GGCTNNANAN	AAASATTTC	YYCNNAANKK	YYTCSGGCTT	CYKNGHMRNR	GMCAACCCGR	1080
GS						1082

(2) INFORMATION FOR SEQ ID NO:300:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

AATTGGCAAG	AGTGATCGCG	CTGAAGCGCG	TAGCGCGCGT	GGCTCGGGTG	GTTCGGCAAC	50
AAATCGCGCT	CGANGTGGTC	TCGGTAGCGG	GTGTCCAAAA	CGGTGGCGCG	GTGCGCGCGG	120
ATCTGATCGG	CGCGCGCGTA	GTGCACGTGC	CGCGCGGTGT	GCAGTCCGAT	GGCGGAATGC	180
TGTTGTGGT	GTGTTGACCA	GCGCAAGAAC	CGGTGCGAGT	GCACCGCGGC	CGCCTGATC	240
GACTCGAACC	GTTCGGGAA	ATCGCGCGCG	TACTTGAAGG	TCTTGAAGTG	GGCTCGAGAC	300
AACGGGTTGT	CTTGCTGGTG	TGCGCGCGTG	AGTGCAGCTT	GGTGACACCG	AAATCGCGCA	360
NCANCAATGC	CACCGGTTTG	GACTCATATC	ACAACCGCGG	TCCGCGTCMA	GGTCACTTGT	420
NCGCGCGTAA	TTTNTGGCG	GGCAAGGTTT	TGCGGAYCAN	KCGCGTCGCG	CAAACTTCG	480
ANTCNCGCCA	AGCGGCGCAT	CGNCCCAAC	AMGTTACGGG	ANAAANATY	CAAGAYCAC	540
CTTCGGGKIN	TTATATCTYC	CCYTTGGSTY	GGCGCGCGCG	CYTTGGGATY	ACCGCTTCCA	600
ANTCGCAACN	CGCKGCLANA	RCYGGGGGCG	CGCGCGACCG	CGGKGDAAKA	WTAATTTAAA	660
CGCTAACMAW	ACTTMMMACC	CNNGGGCGCY	AACGCTTYNR	AGGTTTTTCT	NAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAACCGCK	CGNWTCCCTC	CRASATTGSC	NCGBAAWESA	780
AKGCGCGGNY	TCGCGGNNMC	CGCGGGKKTG	KGCTTCCGCT	WMCNMYWTS	GGCGNACCGN	840
CTYSSMYGCG	CGCGCTGCGH	CTCGGKKTCC	CGACCGYANC	MGCGCGGCTM	GGKCGCGWGT	900
YKCGCGCGCG	AMNNNGGGG	GGACCGTNGG	CGCGMKRSGH	TCCGNAITGA	MCCTGNGHKA	960
MKCYCNGEAR	AMCCGCGCC	MGCGNCKCKN				990

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AATTGGGCTG	GCACCGCGCG	CGTGTGCGCG	AACCGCGCGG	CGGTGCTGCG	CGTGGGCGCT	50
GGTGTGCGCG	CGCGCGCGCG	GGCGGCTAAC	CGCGGCTGCT	TGGTCAATGG	GGCGGCTGCG	120
GGCGGCTGCG	GTGTANGTGC	GGCGCGCGCG	AACCGTGTGA	CGCGGCTGCA	GGATGGGCGG	180
CGGTGTGCTG	CGCGGCTGCA	CGACGCTGCT	CGCGGCTGCG	CGG		223

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

AATTGGGCGC	GAGCGCGCAA	CGGTGGCAGC	GGCGGCGAGT	CNGTTGCCAC	CGCGGGGGCG	50
GGGAACCGCG	GTGCGCGCGG	CGCGGCGCGG	GGCGGCGGCG	TGATCGGCAA	CGCGGCGCAA	120
GGCGGCGAGT	CGCGAATGGG	CGATGCGCGG	GGCGGCGAGC	GGCTGCGCGG	CATCGGTGGG	180
CTGTTGTGCG	GTTCGAGCGG	GGCGGCGCGG	CGCGGCGAGC	CGAACCGCGT	CGACACCGCG	240

CAGCACAGGC	GTTCGGCGCA	GTCAACGGGC	CGATCAGGC	CGTACCGGG	CGCCCTGAT	300
CGGCACGCG	CGAACGGGC	CGCGGGCAAC	GGGGCCCGG	CGCGGACGG	CGGGTGGTTG	360
TTGGCGCGG	GAGGAGACG	CGGGTCGGC	GTCAACGGC	GGGGCGGGG	AAATCGG	420

(12) INFORMATION FOR SEQ ID NO:303:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AAATCGGCAC	GAGGGGACG	ATCGATACA	CGCGTCGGG	CGAGCCGGG	CGATACGCCA	60
GCTCGGCACA	CGCGAGGCCA	CGATACGGGC	TGTGGCTGTC	CGCTTGAGC	ACGAGCGGCT	120
TACCGGCGAC	CAGCGCGGGC	ACCGAGTCGG	ACACCGTAAG	CGTCTGAGG	TAGTTCGACG	180
CGCGATCGAC	CGCCACACG	CGTTTGGTT	GATAGCACAC	CGTGGTCTTG	CGATCGCGG	240
CGACGACGGG	CTGTGCTTA	CGGGGCTTGA	CGAGGTCCAC	ACAGACTGCT	CGCTTATAAT	300
TCGCGCTTC	CGATCAGAT	CGACAATTTC	CTTTTGGGG	CGCCATCGGG	CGTTTGGCGG	360
CTCGGCTTGG	AGGAAGTCCA	TGAAGAAGTC	CGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
CGCGATGACT	CGAGCTGCT	CGATNACGGG	ACCTTGGCCA	GTGCTCTG	CGCGCGGAG	480
CTTGGCGGAA	TGCGGCTTC	ACTTGGCGGG	CGGTGCGAAC	CGAATCTAT	CGCGGTTGCG	540
CGCTTAAAC	TGCTCAATST	CGTGGTGA	ATTGCGCAAC	TGCTTATGCC	CGCGGTTGCC	600
ACGAGNACAA	ACCTGCGCAA	GCTTAGGTT	TGCGCGGCT	TGAGAAATTC	CGCTTTTGGG	660
CGAATTTGCG	CGCATAGTG	CGAGGCTTC	CGAANAACG	CGCTCTCTT	CGTGGGCGAC	720
CGAAGGGGT	TGCGGCGAG	CGGNNCGAAN	CGTACCGCT	CTGAAGGNN	TTGCGCGCGG	780
CGGAGKKGGA	ATTCGCGGA	CGGCGGCGG	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	840
CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	900
CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	960
CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	1020
CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	CGGCGGCTC	1049

(2) INFORMATION FOR SEQ ID NO:304:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AAATCGGCAC	GAGGGGACG	AGAAATCGCG	AATGGTGAAG	CGTGGTGGG	TGCGGTTAGG	60
CGAAGATCTA	CGGTGAGCGG	CGGCGGCGTG	GGAAATCTGA	CGGCAACCGG	CGAAGGGGTTG	120
AGGGCTGGGG	TGGAATAACT	GAAGGTTACT	CGGATGGAAA	ACCGGCTATT	GATATGTATT	180
GGCGGATCA	AGTTGCTGGG	AATGGGGGAA	GGCTGAGGGG	GACCTGTGGG	ATTGGGGGAA	240
TTGTGTGGA	CGAGAGCGGC	CGGCGGCGGT	GATGGGTTTG	TTGAATTTT	GTGGCGGCGA	300
CGAGGTGATG	CGATTGATTT	TGATGGGGCC	BATCGAATA	TTGGGTATCG	CGAGCGGCGA	360
CGAGATTGCG	CGAGATTGCA	TGGGGCGGAC	AACCGAGGTT	CGSANGTAAG	CGTTTCTGTT	420
ATTTGATGCG	CGATTGCGCA	ACTMTSTGCA	TGCGGCTGAY	MTSATTGCGG	NACGCGGCGG	480

YTTATTTCMS	GCTNAYGGGA	ATBAMGGAA	CAATNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CCTGCTNSYC	CMCCGCRCHC	AKAACCCRTT	KCTGTSTTMC	CCSMAAAATNA	CBCCCTSTTS	600
NACTCCNCSG	AANTNSCCCC	CCCSCHWNTT	ATSTYCCCGK	GTTCGCCCMC	CCCTTMAAMC	660
TCCCGCGTTA	ACCCGCVWTF	SNCCGCCGCS	YTAADMKCRG	GCTTSTTNT	CCGCCYTRMK	720
CCGCCGCTCK	SAMCMWCHC	CTCXAAACAC	CCSCYTKOSH	TMCOCATNT	MCNWCCKCHS	780
KCTNTMCTCK	CCMAYTTCRC	CCNCTCTCC	CCSTSTCAN	WTATAAAACC	MCNYANYTMR	840
KCMCMWMTA	MWACWCTCNY	NCCGCMCNCK	NTTCTAMWC	CMGCCCKSSN	TWCYCKSCCC	900
CCMTCTMNA	CCGCCCKRTY	NKMWCCCTTC	CCGCCCTCCC	MCNBMKSTST	YCSKTNMCW	960
NCNTNTMTCN	CYNANMCKCK	KCTCTCTCCN	CRCTCTCCCC	CCWCCCCCVV	KKCTCTSKCC	1020
CNCTCTCCSC	CMKCGSC					1036

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

AATTCGGCAC	GGATCATGGA	ATAGCGGGCT	GGTCAGCACC	GAAGTGTGTC	GGCATCTGTC	60
GAGCAAGTCT	CCTCTGGCTCG	CCGACGAGGA	GGTCGGCAGC	GATCGCGACA	GGTCGGATGT	120
CTTGGATGGT	GTTCAGTTCG	AGGTAAAGCC	GACGCGCGAG	CTTGTCTAGC	AGGGTGTCTT	180
GGCTCTCTGC	ACGTGAGGTA	ACCAATAACT	CCGACGCGAG	CCAACTCGCG	CCCTCGATCC	240
GGGTACGACG	CTGGGCCGGA	GGCAGCCGTT	GTGCCCCCTT	GGCCGAAGCT	CAGCTCTGCT	300
GGCATGGAAG	TAAGAACAAC	CGCGATGCCC	GTGCGCAAGT	ACGACTGACC	GAGCAAAAGCA	360
ACCATCTCTG	TCTTTCCGCT	GGGGTAATC	GANCCGAGCA	ACCGCAGCGA	CCACCAATCA	420
TTGGGATTCG	CCCACTGACC	GACCAACCGC	GTGTGCGACA	CCCGAGCGGA	ATTGGTGGTC	480
TTCCGCGCGG	CCGMAACGG	AATCAGCCG	ACGCGCTGCG	CGAASCANCC	GCATANCCTT	540
ACATANCAC	CGMTCTGCG	CCGCAATTC	GGGCTTMTGC	CCCTTNGCAA	CCSMAAYNCC	600
CCCAATTCG	AACMAAAAJA	TTGTCCTATY	ARNGTTCCTN	CCAAAACCTN	ANTCCCTCTA	660
TCCCGCGCGG	GGGCCCCCTY	NMMAAAGCG	CCWMAANCC	CCSGGCGSCC	CGGCTTWTTC	720
CCCTCTCTGC	CGCCNCCSCG	TTTGGTCMCH	GGSCMMTNWN	GGGTTGCBCC	CCGCTMAAAA	780
AAAAAYCCKG	NCAATYAAJA	CCGYCMAAA	ASKTGCGSSC	CCCMARCCCG	GGKAACKWAA	840
ANTTAANCEN	KAJAAAAAWN	NCANMCCCC	MGGNGCTTAA	GGKYTTAAGG	GTSTTNMANG	900
AAAAATMTC	CANATMNSK	TTNMAAJAAA	ASCCSWAKCC	CCCNHNKKNK	CCAAWAAARR	960
SGCTCTCGGG	CMWNSGGGGG	KKKKXTNCS	KMBNXTTNGR	CCCNCGGCTN	NNTWECCTTN	1020
TCCNYGGGCG	RNCACN					1036

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

AATTCGGCAC	GAGTGGATTC	GATCGACAC	CGCCGACCT	GGCGAGCGCA	GATCGGCGCG	60
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GGCATGGGCA	ACGGCTACTC	GGCCAAACCG	AATCCATTGG	GGGTCTCACC	GCAACCCCGG	120
AAACCGGGCA	CGGGCGGATC	GATCAAGCCG	CGCACCACAG	ATCCGAAATA	GGCTCCACAT	180
AATGAGACAC	TGGGCGAAAG	AGCTTGACAG	GGCCCGCACC	ACGCAAGCTG	TTAGACCTGT	240
CGGTCTTGCA	AGAAGCGGGT	TGGCCACCTA	AGATCACGCC	GGCCAAAGGC	ATCGAGTCAA	300
CGTTCGGGTG	GTACCGGCT	AACCTTGGCG	CGGCCAAGAA	ATGACGGTGC	GCATTACCAT	360
GGCCCTTGCT	ATGCGCTTTG	GGCACCTTGG	CACCAAAACT	ATGANCAGCC	TTATGCCGAG	420
TCTCTGGGAC	ATCGGCGAGC	GCTTCAAAAA	CTGCTTGGCG	ACAATGCTAT	TGCTGANCCT	480
CGGAATTTCT	NTCTTGTCAG	GAACACTTCA	TGTTNCGGTT	NAACAACCTT	GCTTGAAGAA	540
ACAGCCATA	TTGAATTCCT	ANTCGGGGAG	GAACCTGTTT	CGGAAGKTGG	TGGGAACGAA	600
TGCTGCCCAA	AAATCGGGGG	NGGTAAAGAA	CCGCSNATGG	MSAATTTTTC	CTNGAACRAM	660
AAAAGGTCCA	AGKYCAAGAG	NGCCCCCCCC	GGMAAATTTG	TGAACSCAKA	NYANETTCCT	720
WNTTNCAAAT	MTTNGGGTCC	KNTTCCCCCT	AAANGGGGCT	CGCCNCCCGG	GGTTCCTCCC	780
NNNNGGGGNN	CYTCGCCCCA	AAAAAAMMM	MTTTCGKGG	SMGGKKCCCC	CTCGGTTWGG	840
GKCTTTAAAC	CGGKGGGCTN	CAAAAAANAN	ACCCGCCGMS	NGGGGGGAAA	ATTCTNAANT	900
AAGGKKKCTC	SCMACCCCAA	AAANMMNNCN	ANMCCCGMK	SARGGGGGNY	TTMKAGGGMG	960
GYCCCCCGCN	YCGGGGGGNA	NAAYAAAAAC	NGMGGGAAT	NTTNTTTTTC	RSSSRNKTTC	1020
TYTCTCTYCN	CGMGNRRWNG	SRAMNTGKTS	NSGGGGGGCC			1080

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	AGGCTTCACC	AAAGAGTTGA	CATGCGGGGT	GATCGGCACAT	CGCATCGAGG	60
GCATATCGGG	CATGGATGAG	CGGAANGGAN	TGTGCGCTTC	GCTCAACTGG	ATTACGGTTC	120
CGAAGGTGAA	ACGCTTTGGG	CGGAAGGATG	CGAGCTTTAA	CTTGGCGCTTC	CACCGTGCAA	180
TGTTNGTATG	GATGCTGGAA	CGGCGCTGAC	NGATAANGAA	TGTGCTGGTC	CGCCGGGCACN	240
ATGGATGGTC	CGSTTTTTCN	TCCGCGGTTA	AATTGCTGT	GCATCATCTG	CGAGGCTATG	300
TTCCCGCTAC	CTGCGAGGCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAGTC	GGGATGACNC	CGGGCATTTC	CGCAACCTGC	TGTGTTTGA	GGTMTCAAC	420
CGAATCGGGC	GCTTAAAGGC	NGGCTTGGCT	TGATTMAAC	CNAACCCNTH	CHATYCTTTG	480
CGGNGHMTG	GCTTCTCTCC	AACCTCGKKG	SYTGCCNCGG	TGAACCCGNA	CTNCCGCCCC	540
GTTGGACTTA	MRTNTTCAA	AAMCGGTHNA	ACCGGAATNN	SACCTNCCG	TCAAATTAAM	600
SAATTCGGGC	TTYGGGWRCC	CGCCNGAAYW	TTNCGNNGGG	GGNTYCTCN	GTTTYGGGGG	660
SAACCTTTTG	CGCTNCCMN	TTACAMGGC	NCMTNMTTGM	GGGSCNNAS	GWCCCGGKKG	720
TNTTNTCAAN	TGNCNNTTTT	TTGGGGGGGG	GGGYRTTTC	NGGGCCCCCG	GGCCCCGMAA	780
AAAAANCMGA	RRCNCYGGG	KKCCCCCGCM	NNATNGGGGG	YKCAAAACAA	ACCCCAANBA	840
TNCGNMGGGG	MACCCGNNGN	GYZAAAKGCT	TSMCTMAMN	KKGMANNCT	SGMSCMNNN	900
KTGGMGGGKT	TKGNNGAAN	AAANMKGGM	RCGNCNCGNN	GAAGCGGMS	GGSCCNGN	960
NKASNGWNG	CRNNGARRCC	NCNGYEMRN	NGGNNNGNN	CGGRNNNAN	NMCMCAWMC	1020
NEHMGNNNS	CGYMTNCCG					1080

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGACAANGG	CGTGAATGCG	GATCCGGCCG	AGCTGGGGCC	CCTCCTCAGC	60
CACCTGTGCG	CCAGATCGCG	GGCCACGGTT	CGGCTCTATG	GGGCTAGTT	ATCTGGCCCG	120
AGCCTGAAC	CAGGGCGAGA	TTTCGGCGCT	TTTCTCGCC	TGGCTTCAGC	TTGGGGGAAG	180
TKGGGAACGG	TCAGGCTTGG	CAACCCACGA	TCGGGATCGT	GGGCTCGGTC	CAGGACTGGT	240
NTCTCTGATA	CTTGGGTACA	TCGTGACCAA	CTGTGACCAA	TATTGGGGCG	GCTCTCTGTC	300
NGTCCGCTCC	CGCGCGGTAA	GGTCCACAC	TTCTTTTTC	TCGTGCGG		348

(2) INFORMATION FOR SEQ ID NO:309:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 312 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGAGACCGG	GTCTTGAC	AACGGAGCGT	TGGCGCGCGG	GGCCTTGCGT	60
GGCATCAGCG	CTTCTCTCTT	TTAGCGCGCT	AACGGCTGCG	TGCTCTTTTG	CGGCTCTTGA	120
CAGCCTGCGT	ATCCAGCGAA	CGCGCGATGA	TCTTGAGCG	CACACGAGCG	AGGCTCTTCA	180
CGCGCGCGCG	GGCAGCAGCG	AGCATCGAGT	GCTCTGCGAG	GTCTGCGCGG	TCGCGCGGAA	240
TGTACCGCGT	GAGCTCGAAC	TGACTGCTCA	CTTACGCGCG	GCACCTTTCG	GAAGCGCGGA	300
GTTCGCGCTC	TTGGGAGTGG	TGGCTCTGCG	CG			312

(2) INFORMATION FOR SEQ ID NO:310:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 942 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	AGTCTGCTCT	AGACGATTC	AATGCTCGCG	CGAGCACCTC	GGCACTGCAC	60
ACGCTCGCAG	AAAATGTGCT	CAATGTGCTG	AACGAGCGCT	TCCAGAGCGT	CACCGCGCGG	120
CGGCTGATCG	GCACCGCGCG	CAACGGGACT	CGTGGAGCGG	GGGCTGAGCG	GGGCGCGCGG	180
GGTGGCTGTT	CGGCAACCGG	GGCAACCGCG	GGTCCGCGCG	GAACGGAACC	AACCGCGCGG	240
ACGTGGGGAC	GGCGCGCGCG	GGATTCTCTC	GCACCGCGCG	ACCGCGCGCG	CGGCGCGCGT	300
CGCACACCGG	CACCGCGCGG	GACCGCGCGG	CGGCGCGCGG	GCTTCTGAGT	GGGCTCGCGG	360
GGTNACCGCG	CACCGCGCGG	CGGCGCGCGG	CGGCGCGCGG	GCCTCTGAGT	GGGCTCGCGG	420
GGATCTCTCT	CGGCGCGCGG	GAACCGCGCG	GGCGCGCGCG	ACATTAGAGC	CGGCGCGGAC	480
CGGCGCGCGG	CGGCGCGCGG	GGGCGCGCGG	CGGCGCGCGG	CGGCGCGGAC	GNNCGGCTGT	540
GCTTGGGGA	AGGCGCAACT	CGGCGCTAGC	GAAATCGCGG	AGGCTGAGAC	CTATGCGGCA	600
MYTNACGAA	CTGCGCGGCT	CTTGGGAGCG	CGGCGCGGAA	AGGCTGAGAC	CTATGCGGCA	660

NNINCYTTTNN	MATTKGGNNNA	AAAAACCCCTY	CCWCSGRACT	NCCCCCOCNOM	GRMCNNTNEN	720
NTTTCGNCNN	CCCGGSNAAM	RMTTKATTTC	NGGGGGNTCN	GGGTOMNNNA	AACCCCAAM	780
MNNWNCSCA	ANGGGSNGC	NKNNMNSGT	TTTYCKMRA	MNNWTTNNNN	NTONGARSEN	840
NAAMCNRNEN	NGKKGNNRAA	ARNNTTWTN	KNSCHNNCN	GRNNVVRGGC	CKMSSGNNNG	900
MCWNSHNRNG	MNNSCNCNKC	NNNPNAAAAA	AASGVNVCYS	MSNNKTKKKS	NNGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTGCGCAC	RAGAGAGCCG	CGGAANGTTT	CGCTGGCTC	TACAACCTCA	TCAAGCCCA	60
GGGGGAACGC	AACTTCGGCA	AGATCTACGT	TGCTTCCCG	GAAGCGGTCT	CGATGCGCCA	120
GCACCTCGCG	GCACCGGACG	CGGAGCTGAC	CCAGGATCG	CGCGGSAAC	GGCTTCGCTT	180
GCAGAAGATG	TGCTTCGAGG	TGGCTGGGAG	GATTTTGCAN	CGGACGCCNG	TGACCGCGAC	240
GGGTTTGTG	TGCGCACTGC	TGCTCAGCAU	CGCGGACCC	GGTTTGACCT	CGACGAGCTG	300
CACCACTGCT	CGCGCTGCTG	CGG				323

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTGCGACT	GTGTGTGGCG	CGCTCCAGAA	GAAGATGATC	CGGAACATCG	CGAGCCCGCG	60
CGAGGCTATG	GTGGCGGTGA	TGGCCGACCA	CGCGATGATC	ACCGGCATAC	AGCCGCGCGC	120
CGACGCGCAC	ACCACTTCT	GTGAGCTGGG	TGGCTTGAAG	CAAGCGTGT	AGACRAACAC	180
ATAAAGCGC	ACGGTGACCA	GGGCCAGCAC	CGCGCCGAGG	AGGTTGGTGG	CGCACCATAG	240
CGAGAAGAAC	GAGATGACCG	TGACGCTCAC	CGGAGTGCCA	ACGCGTTTGG	GGTGGGCGCC	300
CGCTTCCCGG	CGAAGGCGCG	CGCGCGGGTT	CGCTTCATCA	CGTTGTGAT	ATCGGCGCTG	360
CGACGACGTT	GAGCGTGTG	CGCGCGCGCG	CGGCGATCAT	CGCGCGGACN	ANGGTTTGA	420
CGATGACGAG	CGGATGAATG	CGCGCGCGCG	TGTTGCGGCT	CGTGCGGAT	TGACGCTGCT	480
CGACGACTTG	CGGCGGCACT	CGGAACCGCG	TGAATGANTG	AATTTAAGC	GSTSAACANT	540
AACATACATA	CGGTTGGGGG	CTTTTAACCG	GTYYTGAANG	GGTTTTTTTC	TTRAAGGAAG	600
AACYATTTCG	CGATANTCTG	CGTTNTATCG	GAAGAAGCGC	CGCCCATNCG	CGTCCACACT	660
TTSCCGCTGA	ATGGGSAATG	MNCGCCYKIR	CNCGGNCCTT	AACRCGCGCG	CGWTTTTTGT	720
MCCGNCCTKA	CNTTMMTGC	ARNNCGGCGC	SKCCCTTCCK	TNTTGGCTCG	NTCCGCGNET	780
TNCGGTCTCC	CNNAMNTVNA	ACCGGGGGCG	YINGGGKCRM	TWTGKTITGG	CGCCCMCCCG	840
MAAANASAA	GGGGKRMSTY	CGTTGGGCGC	CCGMAAARGG	NYCCCGCGAM	YTNKZKMSY	900
CNNTKNGGNN	CTGTNCRNGC	GAABAMAMCC	KCCCGGNETS	STTNTYVWAG	GNRWKNGERG	960
CGCCCGGGGY	MNNNAAYANN	MNNTATCNS	STNANMAKEN	NNNNNNNSCN	MNNGNNNTCN	1020

SCNSNGGKBC CCCC

1034

(2) INFORMATION FOR SEQ ID NO:313:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTGGGCAC	GAGCCACAT	CCGGGGCCGC	TCCTTGCATG	ATCTGTTGTT	CATCGTCGAC	60
RAAGCCACAT	CCCTGGAGCG	CAATGTGTTG	CTGACCTTGC	TGTCCCGGTT	GGGGAGCGGT	120
TCCTCGGGTG	TGTTGACCCA	CGACATCGCC	CAGCCCGACA	ACCTGCGGGT	CGGCCCCGAC	180
GACGGGTGCG	CGCGGTGATC	GAGAAGCTCA	AAGGTCTATC	GTGTGTTGCG	CACATCACTT	240
TGCTGCGCAG	TGAGCGCTCG	CGATCGCGCG	CGCTGTGTAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCGC	TGAGTGGCGC	TCCTCGGAGC	A			331

(2) INFORMATION FOR SEQ ID NO:314:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTGGGCAC	GAGATGCTCA	CCCTGGCGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTTAC	60
GCTGATGGGG	CAGAAGATGG	ACCAAGTGCT	GGGATCCCGG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGATCG	CGGGTCTCCA	GCTACGGCGA	TRAGCTGGTG	TTCCGCATCA	CCGCTGACTA	180
TGACCCCGCG	TCCGAAATGC	AGCAGCTGGT	CAACGGTATC	GAACTGGGTT	TGGCCGCTCT	240
GGTGGCGGTC	ANCGACAATT	CCCTGCTGCT	GTTTACAAGG	ATCGCGCTAA	GGTTTCATCC	300
CGGCGACTTC	CGANCGCCGC	CGGCGCGGGG	CGGCGCTCTG	TGCCGACCGC	CGGAGCGCCT	360
CAGTGAAGCC	ATTCCTGCTG	GCCTTAACCC	CGTGAGAAGG	TGGTCTGTGC	GCAAGTTGGG	420
CGCGGTCACT	ATCATGCTCC	GGCCCATAGA	CCGCTGTGCT	TTCCACACCA	CNTSNGACNC	480
CCCCCAGGAA	CTGGTCCGGC	AMTNCAGGAA	NTYCGTGTGG	GCACCGGCTT	CTTCCGCTRT	540
GGCTTAACAT	TCCCATTTTN	CGGCGGGGCT	TGGCGTTTNC	GNCGGGGCGG	NTCTTNCGAA	600
ATCGGCGMAA	ATCCCGAMMC	AAACCCCGCG	GCTCTTGGGG	CGCGGGGCGG	GGCCMAHNCG	660
AAACCCCGCG	NTTAAATGCT	TTGKTGNCNN	CHCSGGCMCC	NCHAAHSCAN	CCCTTTTGGC	720
NCCTCCCGCG	CCCAWTTTAA	CCGAKCGGCH	AAACCCAGGY	TMGHGGCYCY	KNAAAAAATA	780
AATTGGCGCG	CCCCAANTAA	ATTCGCGGGC	CCYTTGGGGG	CGRANCFMYT	TTTMCCHSSS	840
TKGNNAAMC	MGGANCCGGG	KAAYTMTMTC	NAAYCGCCSN	AAMNTTTTTC	TAANNCCGCH	900
YNCCCGGAAA	ATTNAMAAM	CMNKTGNSG	GGGCKTTGNC	SGKKGRADGM	AAAAAANREN	960
SKTMTMCHNN	SANMCHNNNN	SGGNNNNNNN	NNNCNCGYKC	CSNAAMHCCC	CGCGGGGGGG	1020
CGMMCC						1026

(2) INFORMATION FOR SEQ ID NO:315:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTGGGAC	GAGAGAGCG	CCGARNGTST	GGGCTGGCTC	TACAACTTCA	TGARGGGCA	60
NGGGGAACGC	AACTTGGGCA	AGATCTACGT	TGGCTTCCCG	GAAGCGGTCT	GGATGGGGCA	120
GTACCTCGCG	GCACCGCAGC	GGAGCTGAC	CCAGGATCCG	GGCGGAAAC	GGCTTGGCTT	180
GGAGAGATG	TGCTTGGAGG	TGGCTTGGAN	GATTTTGCAN	GGAGCGCCNG	TNACCGGAC	240
GGTTTCTGT	TGGCACTGC	TGCTACCCAC	CCGCGGACCC	GGTTGACGC	TGACCAAGCT	300
GGACCACTCG	TGGCGTCTGT	GGC				324

(2) INFORMATION FOR SEQ ID NO:315:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTGGGAC	GAGAGAGCG	CCGARNGTST	GGGCTGGCTC	TACAACTTCA	TGARGGGCA	60
GTAGTGGGCG	GGTGGGCTC	GTGCTTCTC	TGACGGGCGC	GGCGACUAT	AAGGTGGCTM	120
ATGCGGAGGT	AGCGGCGGAG	GTGCTTCTC	TGATGATGA	TGGCACTTTC	CAGCTTGGCG	180
ACCGGAGGCT	TGGCATGGG	CTTATCAGC	CAGGACGGCT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGCT	CCAGATGGC	CTTCACTTC	CAGGCTGCTC	CAGCGCAAT	GGTTGATTT	300
CTACTGGGCG	TATGCTTCT	GCATCGGCTG	GGGATGAAT	GGGAACTGCA	GGATGGGAC	360
GAAGGGGTCT	GGTCTAGCT	TGCGGCTTT	GGGACAGTG	GTGACAGCC	GGTACTGGCG	420
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	480
GGCGGGGCT	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	540
GGCGGGGCT	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	600
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	660
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	720
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	780
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	840
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	900
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	960
ATATATGGG	CCGAAATCG	GGCGGAGCG	GGGCACTAT	AAGACAGCC	AGTAACTCG	1020

(2) INFORMATION FOR SEQ ID NO:317:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTGGGCGAC	GANGCGGTGCC	GCINAAACACC	AGCCCCGCGC	TGCCAGATAT	CCCGGACTCG	60
GTATGCGCGC	CGGTGGCGTC	GTTCCTCTCC	TGACGGGGCG	CGCGGACCAT	AAGGTGGCTM	120
ATCGCCAGGT	AGGGGCCGAG	GTGCATGGAG	TGATGATGA	TGCGACTCTC	CAGCTGGCCG	180
ACCGGGAGCT	TGCATGGG	CCTGATCAGC	CAGGACCGCT	AGGACAGTC	GATCGAATGC	240
ATAGTGGCTC	CCAGATGGC	CCTGCAHTC	CNGGCTGTCT	CACGGCAAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCGC	GCATCGCGTG	CGGGATGAAT	GGGAACCGCA	GGTACTCGGC	360
GAACGGGTCT	GANTCTAGGT	TTGCGGCTTT	CGCGACAGTG	GTCAACANCC	GGTACTCGGC	420
ATATATCTGG	CCCAAAATCG	CGCGCGACGG	CGCGGACNAT	AAACACGGGC	ACACACATCG	480
CGCGCGCGGT	CACCCAAACA	ACANCTTGGC	ATCGGATTTT	GTCCCGMCGC	CTCAACCGGT	540
CGCGAAGCCG	TGTCGCGCG	NACTTTTGCT	NWNTAACTG	CGGCTTCGCG	CGCTGGNGCA	600
WTAATTTGGA	AACCTTTNCG	CCACTTTGAA	GGGGTTGTTC	NATTTTACTC	GTAAACCGCG	660
AATTTTTCGG	GATTCGGTCH	KCGGGGTITT	YSTTTTCCCC	ACCTTNGNAN	GGGCGCGCGA	720
AGSTTTTCTT	SYTGAAGGCG	GAACCCCAAC	TTTNTTYYN	AACCTCGNAA	NYMTTTCYCG	780
NNAACCGNKT	CGCTTTTAAC	CAMGGGGGTN	AACCGTMMNG	NGGKTAAGAA	GGGSKMKTG	840
NCCCTTMMNG	GGGGGAAAA	TSTKTCNCG	GGGCGCAAAH	ACCMNMYGH	GTGKKKFKS	900
CCGAATTTT	NMMAACTT	GGGGCCSGA	NNTTTAAAG	MSCCGGSHN	GTGKCCCMN	960
NTTTCMNAA	WHKXKXMM	SNMNSGNG	GKYNSSGSHN	NNAAGMGGG		1020

(2) INFORMATION FOR SEQ ID NO:318:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:318:

NGNGGGGWNH	HTCAYCAYCA	YGCSSGGGYW	ENATTGCGGC	CCGACCTTGT	MAASAGATCT	60
CSAAATTCGGC	AMGAGGGAMT	CKCTMNCNCC	CGCTGTGCAAN	CCAAATRAGGC	CTRATAATTT	120
CGACTCCACA	AAAAACCGTT	GTGTGTATTT	SCCGRAAATR	AAGGGCCCGG	TNTCAACWYC	180
CGCGGTXTTY	CGRATTCGCG	TXTTGTAMCT	CGCGGGGTSR	AAAYCCCGGG	TUTTGGAYCC	240
CGCGATTTGAA	ACTCGCGGCT	TGAAACTGCC	GTTTTGGCSA	TCCGGKWATT	GAMCTCGGG	300
ATTAAAAAAC	CGGKTTTNGN	GCTGSGNCGT	CCAAATNCGR	AYCCGATAYC	CAATGGCGTG	360
KYCTTCTCCK	YCGGTACCCA	AACTGCGGTA	TGCTATACCT	GYCCCTAAAK	GCAWYCKGS	420
GCTGYCMHTT	TTGCKGGGCT	CCNAATTGAS	CACGACCGGT	TGCTTTCATA	CCMAAACNCG	480
CKTGGGCGCC	AGMCCGAAAA	AAAKAATAAT	RAKAAKGGTG	CATTCGCAAA	ACGNCGGCGN	540
CCGNANTMCH	ATCGHTNCC	MSCNCCGCCA	UGCGTMAAGX	TKSGGAAYTT	CTMNAACCCC	600
CAAAACCCCA	TACNTMCHG	GAASAAACCC	CTYCNCGGGG	GYCMNCAAA	ACACNCTTAT	660
TTGCTKSTTT	CGGMMCCGT	CGCGCCMAAA	YCCCAAASTA	CTTTTGGGGT	CCNAGAKAAA	720
ACGNCGGGCH	CCMCCSHAA	NWTATYTCTT	KGGCAAMCCC	CSAAACCTTE	TCMNAACNCK	780
ATMTCGCTTT	CGGVCBAAT	TGGYCGGRAT	NCGNCCTTY	TCAAARKKSC	CAKWHNNG	840
GRNMNACCA	ACCCCAAGTY	CCMNAAATN	CKCTCCGCTC	CNAACACGNK	TYTTCSSAAA	900
ABCGCCCGCC	CCGCCCRPA	AACCCCGCNA	RKANTHCCCA	AAACNMYNKG	GGCCCCCCCC	960
CAACCMMAAA	AMCCCCCGSN	RMACSGGGGN	NMCCCCGKKK	KXTTTTCTTT	TKCGMRSCCC	1020
AAMGCAMWXY	ESKTNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNWYRSH	CCGSHWGMNA	1080
GAASMCCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

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GGGGGGGNNN  NATAACATCT  CTGTGACCG  GGGMTCTAKT  GGGGGGGGGC  AATCTGTCTA  50
ASAGATCTCT  NAMTTTCGGG  ACNAAAACCT  GACAAATVNT  GGGGNNMTCC  GTGTCTCTKA  100
TGGCAAAACG  NGTACACACG  ASACACRTAT  GTGTGGCCAC  GACCAATTCX  TTGGGACCTC  150
GCTRACCGGY  TGGCCCNACG  CCACCTTGCG  GWTCTATCCC  RACCGCGGGC  ACGGGYGGGG  200
ATATTGACAG  CACCAAGCCC  AGTTTGGTGG  ACATATGCCC  GGCATTTTCC  TCTAANTTGG  250
TGAACCGGAA  TTCTNMTTGA  ACCNCCAAAG  CCGCCNCCNR  AACATTTTCC  WTCCCGGCTT  300
CTGGGACCGG  KTTTCCGGGG  GTTTCGGCAN  AANCGCACCC  WTGGWTTTCC  TCCCGGCGCC  350
GGCGGACGAA  WTCCGGTTCG  AATTTTGCGA  AYCAGGGGCG  GGATTTCCSCA  AACGGGTGGC  400
GAACTGTCTT  TCRAMACGCG  GGAACCGCAA  TTTCGGGGCC  ANAAATTTTC  TCCACCACTC  450
GCTTCTACTT  CCGGACCTCT  AACMANTTTC  ATCTCTCTNN  CTTCTGCCCC  TGGGGCAGCG  500
GKAARYACCG  GHTTTGGTCT  CCGAACCTGC  GCGCCAAATC  CCNACCCGCA  GTTCTNATTT  550
GGNTCGAAT  GCGCCCGGCT  RANAACCGCC  NTGGCCNNTT  GCGASSAAAA  NGGCGCCCTT  600
KGGGCGCCCC  AGTAANACCC  TACCNNAVTS  CANTTTTTCG  CAAASTTSGG  ACCAANSKTS  650
GGNTTCCGGK  ATTTTYYTGS  GGNCCGCTTN  TATNGGSHTN  GGGGCKCYNC  NCTKTGTGCA  700
NAGSKAYCDS  NGNNGGGGCT  ACCCGCTTNG  GGGGGTTTTT  NBSGCCCCCC  ANAYNKSTG  750
GCGCCCGNCG  GGAAGAATTT  NMTTMCNSGG  GGGAAWTTTT  NTSTGGAMCS  GGGACYCCCR  800
GGGGGTTTTT  TCCCGCNCGA  NNAWANGGCG  GGGGGAANAT  NTGNSGNHGG  KMTTATTAT  850
YTYTCYCTTN  TKAAGSGGGG  GTTTKRAJGG  GGGGGAGAAA  AAAAAAATAA  RAGGYTSTTT  900
TGTNCACTCT  GGNWGNWANE  NAGAKTCTCT  CKXCCGCBGS  SNTTCTCTTT  MGNSSGYGGS  950
GNNGNNDAAA  ACHKSEPMAC  KCSYTTCCCG  CBYCTCCCTC  NCMGGGGYGS  NGSCGNSTYN  1000
GNNKGRKNTA  TNGNMGCTTN  SCCTCNCGCC  GCGKNTGTTC  TMTCNMYGSG  C  1251

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(j) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

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AATTCGGGAC  MGAATATCAC  CAKCTGYGCT  GGGCCAGCAA  AGTGGAGCTA  TTACTACCTG  50
TATGTGATCT  TCRACATCTT  CTCCCGCTAC  XTGCTCGGGT  GGATGCTGGC  ATCGKCTGAK  100
TCTAAGGTCT  TGGCCBACGS  GCTGATCCCG  CAAGCCCTTG  GCGCGAGCAC  ATCAKCCGCS  150
AACAGCTGAC  CTGCGGCGCS  ACUGGGGGYG  GNCATRACT  CCAAGCCGGT  GGCMTCTGTS  200
GTGGCNCAC  CCGTGTCCGA  AATCGAAATC  ASGCGCNMA  CCANMAACGA  NAACTGTCTT  250
CTGAAGCCCA  GTTCAAAAAC  CTCAGTWCCT  GGGCCRACT  CCGCAAAACG  TWCGAGTCKA  300
TCTBAGGSGG  CCGGGTCCMC  TCGAACCGGT  TCTTCGNTG  GTTCAMCCCN  AAAMCAAGCA  350
TTCGCGGMC  CGMTGCTGCA  GCGCGGCAAS  TTTMTACGG  GTCGSGCCNA  CAAATTTGCC  400
GGGACAGSGS  CGCCXCTCNK  GGNMACGCC  TWGCAAAAC  CYGCAACGGK  ATCTTCTCKY  450
NAACNCCGGA  KNCNCGSKT  TCGGGGCTTC  NMSGCBAAK  CCGGNCMBT  CCGAATCCAA  500
TTCGCMRYGG  CTTTYYTCT  CCGCGGCGCT  AARYNGGGY  CCAAGNMMKC  KCCCAMBANT  550

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CCNATCTCGG	NGGTCCCNAN	KYGGCGCTTC	NMAATSAHNA	NMNRGGGTTT	TSCYACCGNN	720
AACCGGNNK	KCCGCKCKT	MAMAAAKATT	RATCAMKNG	GGKCKCNCN	NAAMACCCCN	780
CNCYCNWTC	IMYCSKMG	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMT	CTMTCTCNCI	840
MGCGCCNTN	TYCKSGAKAT	ACASMKCTCC	CGCGNGGCGN	MAAMANKAJA	CTAKCCGYGN	900
CCSNSTHTYN	CTSNMNMNN	TCMMNATC	NTVYKCKNN	KCTMKATNWC	CCCTSKCNCK	960
MLAMTCKTGY	SNMTCTCTCA	TGCTCKKSC	SNMSKPTCK	KSNCNCNWN	CNKCNMKCN	1020
GGNSCTRCCT	TCTGNTTCS	AGCKGSKNG	WACNCACAK	NGWCTYTTC	WGRMKNCKM	1080
TCCKCKWCS	MTMTCWCS					1099

(2) INFORMATION FOR SEQ ID NO:321:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(13) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GNWNTATACA	TCWCTGTGYA	CCSAGGATCN	ANTGGGCGCG	MAAKCTHSTN	CASAGATCTC	60
AAATCTGCA	MGAGCGGCAC	AKAKYSTGCT	CCWACCGCGG	CAYACWCCWG	CNGCGCCGCT	120
CTTTCACGGG	GGCKATASMC	ACCGTTGGCC	CGCGCNGGCA	CCTACACCCAC	CCAGCGCCCG	180
AGCGCGGCDW	TRAMCAAACC	ACCGCGCKTT	TAGCGCGCGG	CGCGCGCGGG	CCACCACCGG	240
CGCCACCGGC	ACCACCGCGG	CGCGCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCA	300

(2) INFORMATION FOR SEQ ID NO:322:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(13) SEQUENCE DESCRIPTION: SEQ ID NO:322:

MGNGSGNKMY	ATCATCWTC	TGCACGSHG	MTOWAITCGG	CGCGCAATCT	TSTMNASAGA	60
TCTGGAATTC	GGCAGAGCA	TCGCGCGGNN	GAATGTCGAA	AMGTCWHTAA	CGGCMATCGG	120
TTGCGCGTCA	ACCACTCTCT	SCAKATCGGG	CGCAMWTYCA	AACCRATTAT	TTGGGVCAGG	180
AAATATTGCG	CKTGTRASCA	ACCTGCAGGG	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	TCGGGCAACA	ASCYCRATAA	TGCGGCGCGG	AMCCACAAAA	CGTGANTNGT	300
TTTTGNCRAA	NGCGGTCTCC	GRAGGGGTGA	ACTGCGGTAR	GCTTNTCWYC	NCCTTRACAT	360
TAAACCGCCC	CGMTCTCTCG	CGCGCGCCAA	ATYCTGTCCC	WTGCGNACCA	YCCGACCTCG	420
CGGTATGGTG	RAACACGTGG	GCRACCGGTM	MGCTACGCKC	TGGGTGATYC	KTGCGMTCCG	480
SKAATTCCGG	GATTTCAGGS	CAMGTTTAA	CCAGGYCCCG	TNTGCTYCKY	CNACGACCCG	540
ATCMWNCGGG	TACCTKTTAA	AATTCTTTCT	GGTGGAAACC	AWYCKMAAAA	NMTNTYCCCN	600
CCCMWNGGGG	CYCGGAAKKT	CNACNTEGGT	NACCCCTNCC	YTTGAATTTT	TCYTNMCCCG	660
GGCCCKAAAS	ANACCGGAKC	CCCGGAAATC	WTAGGCTTCN	TGCGCCSTTA	AATTGNCNYC	720
AATCTKCCAA	CGCTCCCGCG	GCTGSCCMT	TAAATTTCCG	CCCKSCASNG	GAATYCYKSG	780
CGGNTWATTW	CCNCGCTTTT	CYGGKHAAC	SCCGCCGNGN	GGCTVCCGCT	SNNTSGCCCS	840
GCTTGAMNYC	AAAANTHGGG	MMCNAGNCG	SCNAMCCGCT	GKGGGGSATN	TKAAYTCYGG	900
GGGGGTCTNYC	CCGCTCENAA	AAGYGTGCGC	KCGSSCCCTC	CGMAATTTT	CNGGNCAM	960

AGCAGGCGGCG	CTCCCGTTCG	WGGCTCCGCG	SNSMAMAAAN	NKCKCKCKGG	CKGAGZHMNA	1020
MCTCSNGNGG	WTCGCGKATC	NSGNSGNGGS	YGNBSAGWCC	YNVNCGACA	ANC	1072

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

CGCCCCGCTC	TTMMTTCAT	TCATTCACCG	GGMTCTAGTC	CGGCCGCAAR	CTTCTCKACA	60
GATCTCGAAT	TGCGGCMGAS	ACAATSTGGG	GTKGGGCAAT	GTGNGGTGGG	GCACTCTTG	120
GCTCGGGAAT	XCGGGGTAA	CGCGGGGTCT	EATGGGTSTG	GCTAATATCG	GTTTGGTAA	180
TGCGCGCAGC	TACAAATTTC	GTTCGGCAAA	ATATGGGTCT	GGGCAATATN	GGGTGCGTA	240
ACACCGGCGS	TGGAAATTTC	GATATTGGGT	NACCGGTRAY	AAVCTGACCG	GGTNGGGTGG	300
TTTCAATACG	GCTAACGGGA	ATGTSGGTTS	VVYACVCCGS	GSAACGGHWW	YTNGKTCCT	360
TMNCNCTSH	CKSAAKTSM	KMGSTSTYCT	MTYCNMGAS	TAMTYNMCC	CGHAYCKSC	420
WAYCGCTCTG	CATVCGMCMC	SGSGYCTCTA	MNCCACCTTC	NGVYCCCTCC	MMTCYCAIT	480
GMTCGGGTW	CTNTHMGCC	CSGCRVCTG	AMCNCSTSGK	CACGNATMYC	CSACKCTCT	540
MCYMCSCAN	MTTCCGCTCN	CTVTNHCAC	MMCSCTCTM	TCMAACTCKC	CGSGYCKCNC	600
MYCTCTCKCC	AYMMACTCKK	TYCVCMNVYS	VMYCKCKCAG	WYKNCCTCCN	ACTCTMYNTT	660
TCTCTCKMCC	CMKACCHTCT	CTCNCSCCCC	CCACAKAYMC	YAWCMCTTCC	MCTCKACSCC	720
CTYCMNVTCM	MMNCMCTCWC	TWNAKCANCN	TTCTCTCTCT	MMTMCNACKC	WCMNTCNCCK	780
SGACCTCTCT	ACTNMKCTCM	TCTCTTNCN	CTYMMCTCC	MYNYCCCTCC	NMTCMCTCTT	840
CTCTCMNMY	CTYVYACAKC	NMTCCGCCAN	KMCACTCTCT	CCCCCAKMKC	ACNCKCCGNC	900
CTCTCTCTCT	ACTCTCMCTT	ATCTCTCTCT	CNVCMYMKC	ACNCKCYAAT	CNACTMNMHN	960
CCANCTCTCT	CTYVYCNHNC	ACCTYCKCCN	CTMCKCHVNC	NHNCCTVRCCT	CTKCCNCNEN	1020
CTMCMCKCM	CTCTCTCMKN	YCCNCCGCT	CTMKKSTCTC	NHNCCTVRCCT	CTKCCNYNTT	1080
NGVYCMNVYS	CTTCTCTCTT	MCNCTVATC	TCTMKCTCTCT	CNCACVCMAC	WMTTACNCC	1140
ACTCTCTCTG	CKCKCMKCTG	MTCTCT				1200

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

NGNGGNNHNT	CWTACATCMN	TCTNACCGSG	NGMTUWATTC	CGCGCGCCAN	NCTTCTMNAS	60
AGATCTCGAC	AAATCGGCAC	AAATCTCTTT	TSMTAKTCT	CGCGCGGNGC	CACGCKTAT	120
GTGTGCTCTG	GTTRACGCCA	CGCGCGGCGS	CGGCGCCTAC	AGCGCGGGRRA	TSCAGGCGCG	180
CGCGCGGCGS	CGCGGTATAT	RAAGCGCGGY	TTTTTCTATA	AGGCTSCGCG	CGCGCGGTRA	240
TTACCGCGCA	RAYCGGKXTT	TTGGGTCTAT	AACGCTTAAT	GCAACCAWTT	TTTTYCGGCTC	300
AAAACTCTCG	CGWCCANATC	NCGGGYCHCT	RAGCGGCATT	YMGCCAAAA	WNTNGGCGCG	360
AAAAACCKCT	TEVTATTCTN	TGGGTATCTC	GVTGTCTCTG	GCAAAAGCTV	CCCGGCTTAA	420

TCCKCTCCGC	GGCGCGCCGN	AAAAACCACC	AATYCCGYTG	GGGGTGKYCC	CNCAGGCGGT	480
TGCTYCGNGY	CACCTCGCCA	AAYYCCCAWT	AKATTGGGTG	SCYCTSCGG	TSYTYGGGCV	540
CAATTACCCC	CWCGGGMAAA	GREAAAAAAN	ATCMTCCMTT	TGCTCGGYCA	YCTTMTTGG	600
AAAAAGGGGC	ATGGSCCGGT	FYTTTACCT	CAAYCCCCMA	NCMTWACCT	YTCCSCCGGG	660
GGGGNCANAA	CGSTTNGCTC	CGSGGNAECG	TKGTMCCCGN	ATCNAAAGGC	CNGAATTTGG	720
TYPSSTYCNAA	ATTWTWGGY	CCCCGCHTTS	YAAAAACCCA	AAASAXCCCK	YCNAMMYKT	780
NGGGGTYSGG	GGGKYCTTK	SNMTTAAACC	CYCCCCAAAA	YVNSGGGKTT	TCCGCYNNAT	840
KCCAGCCNCK	GGGGGGGANA	AAAAAAAAY	TTYTCCSAAA	ATCCACCCY	TCYKTKSTRY	900
AMACGCCCC	TYMKKAYTC	CKVSCNATTC	SGMTTCMAAA	TYCCGYGGCT	TVTCCCCCK	960
CSGGNGCCCC	AAWTTTKT	YCNANTTYC	CCCNAMNMC	AWTGGGGGKS	KCCATCTCG	1020
SCYTMAANTA	AAAAAAGGG	NKTTTYTCTY	MANAAACACN	GTGKCNCCN	CNAJMAAASH	1080
AKMAAAKAGN	NKMTTKNSA	AANCNCGCC	CTSTYTNVTT	NKTNCKCC	CYGGKGNKGM	1140
SWSWYTTCT	NCCRCGCC	YNYNKTGANA	AAMNCCYCCS	GGSTMCRNAN	ASNMVTTCK	1200
STSTNGMCC	KMBANANAN	MCAMWKWYCC				1230

(2) INFORMATION FOR SEQ ID NO:325:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:325:

NGNGGGHONA	TMAYCWTCTC	ACSSGGTCTA	TGCGGGCGCAW	CTMGTMAASA	GAICTONAA	60
TGGGAMBIAN	GCATMTCMMC	CATATATAAC	CATTGGGTCS	GYWTGCAMCT	GRAAWCTGTC	120
CTTSGKGGCC	TTXACRAAG	GTGGMWTGYT	CHTYCTRAA	SCOOTCRATC	TKCTETATYC	180
CTKGGGCTYC	ACTTTAAGG	SATXSCTGCC	TKTAYCATT	SATGCAAWTA	WTGGYCAWT	240
XTTGCCAGGCC	RACGGCYCT	TTTTCCGCA	GRACATNGA	TTGGAWYCCG	TYCCCRAGCC	300
CGCGCACCAR	ACCGGGCNC	AAAGGYCCCG	GCAAWTSCCT	GGTCAAAAA	TGGTGCAAAC	360
AAAMCHATCC	CGGTYTTRAC	CGCAGYTAMC	ACAANKAAAT	TCCCTGTGCC	GCACAMNMT	420
TYVCRATCYV	CHYCCCCACC	TTRAACCTGK	YTGCGTATT	GGCTACCTCC	CTCRACAGCM	480
YCNCCCTCA	AACTTGGGCT	GACTCCAACT	GGTCTGGYCG	AASGGSGGYT	CAMCGACAAA	540
AACCCCRANW	TGCGCAAAAT	TTCCNCCGCC	CYCGGGAAN	GKTGATMTTC	TCNBRACCSA	600
CMGGGBRYTH	HAACCTGAA	CSSSGSNKGA	MYNSCSCGGA	ANTTTTCCCT	TYNGGCGGRN	660
AAANCTTTTT	AAGGTACCCC	KGNNGGGGG	CCGYTTGGG	AAACAACCC	CHATTGGKTT	720
TGAAATNTT	TKNCCGCCA	TTNCGGGGG	GGGCCCCAMC	CCMCTTTTN	TCMSCHNTTY	780
YCYVCGGAAT	THYTCGCCCG	GAAYVCGGSM	CKGYCCATA	NCCGCMWGG	SKYSTGNSAE	840
GGRATMANWT	TYSTTYVNC	CGCGCNWCCC	CCGKAGCMNT	KGNTGAACMA	AAAKCSCGGG	900
GGCNMYMYNY	YCNHNGNRTT	TNCGSSNMT	TYMAAAMMAN	JGGGKYWTY	CKCKGSCSNE	960
GKTYSGGGST	TTTTCNTTS	GGGSAATYKG	NACCCCKMT	AYCCGGGGGT	MTWYTCGCC	1020
SC						1022

(2) INFORMATION FOR SEQ ID NO:326:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:324:

NNCGNNHNTA	TMAAYCWYCT	NCACCSGGGA	TCWATTGCGG	CCGCAATCTT	STMAASAGAT	60
CICGAAYTCG	SCAMGANCOS	CAWCTATTIS	KGTGRACSCC	ACGACGCGGA	CCTCCGSGKT	120
CKTTCATTGC	AGRGAGGCGK	TGGGTGGCRC	CGGTGGCAAT	GCCACAGCCG	CCCCAAAACN	180
CCGCAAAATMY	CAAAAACAA	CCCSGGGGTA	GTCCTSGGCC	GCCAAATYAA	TAAAGCTRTT	240
AJCKKAGGCN	ACGGCCAAAC	GGYCCCGGCC	AACCAAGGNA	CCTCCCGCCG	NATAGGYCCG	300
GYYGGGGCTS	CKTATYKCC	AACTCTCTAY	CTGACGGGGM	GGYCCGMCWT	CCGCGCTCAT	360
CGGTCTCTCC	TGMAATTTTC	CTCCACACYG	GGGGGGAACY	TTTTTMYCNC	CCPTTSGHAN	420
CACCNAGGY	CAAAATTNC	CGTGCCKYG	SHNCAAYGR	GATTGGGGTY	CGKCTTTTNT	480
TGNMCHAAAC	CCGCTTTWA	CCGCCCHATC	CCYTNAATCC	CCGNNMCMNS	RNGKTTGNSA	540
AJKTNNCCCC	AAATCCCAAA	MTCTTTCGCG	NTTMTWMCY	YYCCTTTCCG	CMCCCMGAAA	600
GGSCRCRCY	TGGGAANTY	TCCCNCAAA	AMTCAMMCCM	TTTCGCCNCA	AGAAATTCGG	660
SACTCCTTTN	TCCNGGSHAM	ATANATYTTT	YCKTNGGSGE	TTCCSMTGNC	AMGAATNTCC	720
GGGGAJAHCC	AGRTNNWTCG	YYYGCCCAAN	NNTYCCYGGG	RMCMYNYCY	TTAAANRASA	780
SAACCCGSGG	GGYNNCCSS	TARCCCGCAN	KAAATTTCCG	CGGSKTTTC	TYNNKJGSH	840
GGCCCGCAAN	ACTMTWATT	TCCCKCGNNN	TTTSYCCCKG	KCAMMAMMG	KNCCTTTTTT	900
YCSMATAMA	CTTNGGKCTT	NTNNYUSGCG	CAAAANAGG	CGCGSTTCN	TTCHMAACA	960
YHTSGGMMMA	BAAKAJAWATA	AWNTKXCY	TGNNCCCGCC	CKCKCTTENN	TNKCCKCSKS	1020
GGGNNNNKKR	SWCTCCWCNC	CKCCNCCKGK	CKKHAITHCC	CCCCCGCCGM	NCPNTTTTAT	1080
CCC					1083	

(2) INFORMATION FOR SEQ ID NO:327:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(2) MOLECULE TYPE: GENOMIC DNA

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GGGGNNKAY	MCAYCWYCT	YACSGGMMN	TAITGGCGCC	GCANNTNNTN	GASAGATCTC	60
GANTTGGGCA	MGAAAAAAGW	GAFTGCTCG	ACCTTMCCTC	CGGGGACGCR	ACCRACAAMG	120
RAAGCGCGCC	ANAAATATGG	CCACAKTTGG	TCACATATTT	ACCCAATTMT	AYCAGGGAYT	180
MCATTTCCGG	GGACCRAGOS	CACAATCCCR	ATSKTGGTTT	GCRAACCCCT	ACCGTCCCCA	240
MYTCGCGCRA	STTGACCAAC	GGCRAAANA	CGGCCRAHY	CTCGGCCCTGA	NCCCGCTCTC	300
GGGCMATAMA	CTAGGCCCAT	TKAACGGAAC	CGNGGCGCCG	NANPTSGCCA	ACAGGTCCCT	360
ACAAAGSGGC	CCCAASYCCG	CCGGATCCCG	TTTCACNCCC	TNKTCTCKTG	CCGAATYCCG	420
WTCCRAATNYC	CCWYGGGCGT	TNCKYCKYK	KYGGGTGCCA	AMCTTGCGTA	TNCTATTREK	480
TCCCTTAATAT	SCNATATCTGG	GCNYCCATTT	NCTGGSNTTC	NATTYAMMAN	SRRCGSTTCT	540
TTCTTTCCRA	AACCGSNTGG	CGCCNNMCCA	AAJAATGAIN	ATAATAATGX	YGGCTTTCAA	600
ACCCCGGCCCC	CCCATTCRWT	CSGTTCCACK	CCCCNNGSGT	TAAGTGGGGA	ATTTYTNAMC	660
YNNRGGCCCT	NATTTSGGNA	AAJACCYCYC	GGGYCTCAAA	CBNTTTTTTT	GSKSNWTCGG	720
GCCTKCTTCCG	CAAAAGCCCA	ATENTYNNYG	GGYCKTNAAA	ACMYGGYCRG	RCCGGAAATT	780
TTTCTGGTTC	AACCCCAACC	TTTTCAASCC	NITTTTTYYY	TGCCSCSMM	TNGSGGGGNT	840
KSSGCHTTCY	RARKKCCCGN	GGGGGNYCYM	CGCCPMNTTT	CTTTTTTTTT	CGGTNNMAM	900
NNTTCTTICA	AAAMCCCCCC	SCDCCGNSAA	ACCCCTNAR	GTTTTTYCPMA	AANNWYNNGN	960
KNCCCCCCCC	MMMAAAAAAY	YCSGCCGNNN	ACMSMNSGGA	MCDCCGGGSN	NTRKTTTTTT	1020
THMGSGYCC	CSMAASYTTT	TKMMAMNNK	GAMNSHTTYY	THNNNNNN		1069

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

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NGNGGGGKMK  MATACATCMT  TTTTCAAGSG  GGATCATTG  CGGGCCGCAW  TCTNGTMCAA    50
SAQATCTTGA  TYTCGGGCGM  NAGCCACGCG  TCCRAAAAA  ACCCRAANCT  CGGGGSKCTYC   100
GARAAGTGTG  GCGCGGCKTR  AATTTAACAA  ATTGATGTG  ANAGTGTTCAC  GCGKXTTACTWT   150
YCCCGGCAAA  GGGGGCCAAA  CCGCAGRGA  SCACVCRATG  GKTGYTGKTS  GNGGGGCGCG    200
CGCGKTHAAG  GGACCTGCGT  GGTGTGCGCG  TNCACAAATC  WYCGCGGGGT  YCGCTGKRAT    250
MCNCAGGGGT  GTCAAAAAAC  GCGAACACGG  CACCCGACCC  NTTTACGGGG  GTTAAANGA     300
AAAAAGGGGT  ATCGCCGCAA  GGGGGCGCGG  NCCCAACTT  CGGTGTGTC  ACCACCGCGT    350
CTCTCTGTG  RAATCGGWT  GCRATNYCNC  CWTGCGCTT  TCKYCTYCT  CGGTACCGAA    400
ATGTGGGTAT  CCGTAATGTT  CGCGTAATTT  GCAATATGCG  GGTGTGCGAT  TCGTGTGCGT    450
TCCAAATTTA  CGACGACGCG  TTTCTTTCAT  NCCAAAAACC  GNTKGGCKCC  NRACCCRAAA    500
AAATGAATTA  TATTAANGGG  KCHTTTCHNA  ACCNCGCGCC  CCGNATTCGA  TYSNCTTCCA    550
NNNCCCGGAG  NGGKTAGGT  GGGAAANYTC  TCMACCTYCA  ANCCCTWARS  TTTTNGRAAT    600
KAAAACCTCY  YNCGGGTCMW  TMAAAAAAMA  NTTATTTGGN  NGNTTTGGGG  MNCKKRGKST    650
SCCAAAATCC  MAAATANTTT  YTTGCTTCH  TWAAAAAACG  YGNCCHNCCC  GGAAAWTTT     700
TTTTGCTTGA  ACCCGCAAAC  YTTTTCGMA  NCGSKTTT  CTYTCGCGCC  ANNTWGGGYS    750
GGGAACTGTY  SCVTNTCTTA  TKTCTYMTW  CMGGGGGGGN  MNCTCMGCC  CCMHTTYCYV    800
NYWTCTTTT  KCCCGCTTMR  NNRANNGGN  YTCYNNAAA  AAGNCGCGCC  SCTCMCCCHA    850
AAANCCGCG  MNARAKTNT  TTKKNNEMN  SKCKNKGSKY  YCCCCCGCC  YNNMMAAAAA    900
AATNYCCGCG  BASANHCASN  NMGGRNRS  CCCCCCGCTT  NNNNTMTNT  TTTTTTCSRA    950
GAGCKCCGCG  MNMAMHENC  GTTTTTKCG  NNNNNNGNN  GGNMNMKCG  CCMGAAMWE     1000
CGKSTCCGCG

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(ii) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

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NGGSSNNKNA  TMCATCWYCT  GYACSGGGMT  CWATTGCGGC  CGCAACTNGT  MAASAGATCT    50
CGAATYCGCG  AAKANACACC  ACCGCGGTGT  MTATACACCG  CAAATGTGCT  GTKTCGCAAR   100
ACCGGAGACG  GCGGGCGCGG  GGGYTCCAAC  GCKTTACTVR  ACCGGGCGAY  TCGTGTGTRA    150
AACCGGTGYT  RAGGGCGCGA  CGCAACNTAA  ACGCTTAKC  CAAGRAWYTG  GKTGGCGCGC    200
AGCGCACTGY  TGTGGYTGG  CTGWYCGGTG  GTAGCGCGCG  TTACGCGCGG  TTGCGGCTYC    250
AMCASCSCGC  CGGTATCGCC  AKCHWTCCCG  CGGCGMRACC  CACCGGCGAC  TTTGRACGCT    300
GCTGCGCAAT  CAAAYCKYCT  GWTGCTTCM  AAACACCACR  AAGCGCACCH  CGNSCACCCNA   350
ATMCGGACCT  TTAAGCGCGA  GGCACAAACCT  NTRAKCNGCT  CCGGGCGRAA  GGTCCGCGCA    400
CGRATPCNAA  AAAAKCNKAT  TTCCGCGAG  AKCAACCCAA  NMCGSTTTCG  TGCTTCGAGA    450
TTGGAACCA  ATTMCGGCT  NCHWGGGAAA  AACASCHKCG  NWTAKCTMGG  CCMCGGCGCA    500

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ATTTCGGRAA	SAACCCCTNY	CCCCGGTTTT	YCTTGCTCMG	GCCCAANACC	CCCCGGGAATC	660
AAAAAAGGTC	GGNCAAAAGG	GCMAAACCGS	SACCCMACCT	WTTCCCTTN	GGGGGGGSCWN	720
CCGKGTTTAA	AKKSCCTCY	CTSCCCAAAY	TGGGKCMAAA	NNGRKTGGK	TTNGGCHACC	780
HTTTCGGGKC	CCGGGKGKGG	NGNYCTMMAA	CGTTTTTTTT	SCCCCYKAAA	NYSCCCGCCC	840
CGSSSCGGCC	CCGGGGGGGA	MNTTTTMAA	GKKTYYCCCT	CCCCMAAAA	ANACCCCTNY	900
CCGGGSCCCT	TTKWAAMN	KCTSCCCHG	GNNGGGGKCM	GKTTATTMT	MNCCSCCCTC	960
TCCGGGSAAA	AAATAKMTT	SYCCCCCHC	CTCCGKCNCR	GRAMSMSCG	TCCCTCTCNC	1020
GCNKHTMAAN	AKSMCKKRN	CNCYKCCGS	NNGKCNWCD	NCCSTSMCT	NEGCNCHCN	1080
KAAAHAAINC	NGSMSTSMN	CNKCC				1200

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGNENKNNK	TMAAYCWYC	TSCACSNQGA	ACNANTCGCG	CDRMAWCTNS	TKKASAGATC	60
TMGAAVTCGG	CAAGAGCCGC	AGAGTGTGT	GCATCTGGTC	ANAGTBTMA	CGCGGTGCCC	120
CGGTGTGKTR	GACACACAT	NTGCGACAC	CAAAACCCCT	GGGGYCCAC	GGCKTGGCT	180
GCAAAVYCT	CCAGGCGACC	TCAACAAYN	YCTYCTGCA	CGCARGCCCT	TYCGGSCCG	240
RATCGGGK	CASYTCGCK	TGGTGTGCC	AAGKTACTGS	CSCAYCAAAA	CCGCTCCGGG	300
RAACRAACT	AANTYTCGG	AATTTCTTC	CCCTCGCCCT	TGATAAAATT	NTNAGCCAC	360
CGCAACCTY	CGGGCTCTC	CTCKTGCCRA	ATYCGRWTC	RATAYCGCCA	TGGCCTNKTC	420
KYCTYCGYCS	GTACCCAAAT	CTTGGCTATC	CTATANTKVC	CGNAAACCA	ANTCTGGGCK	480
KTCATATTC	TGGSKTCRA	ATTTAMACA	NCGGTTTGT	TGWTACAAA	AACCGTGGG	540
CGCCACCCRA	AAAAGKATA	TAATAAKGTG	GNNWCAAAAC	CCGCCCCCG	RRTTGAAVCG	600
GTCCACACCC	CCAGNNGGTH	AGGTNNGAAT	TUTMAACCC	CAGCCCATAA	MTTNGSNAA	660
AAACCCCTCN	GGGYMYCAA	AMCTTTTTG	GGMTTCGGG	CGTKYKCC	AAAACCAAAA	720
TMTTTCGGT	GNWAAAAACC	GGCCCGCCCG	NAAATTTTT	GKCAACCCCA	AACCTTTAM	780
CGNNTTCTY	YCCGCSACAA	TNGSGGKMN	NGSSCTTTT	TTWTTTTYNA	GGGGGGRWC	840
GNCCGCAAN	TYCCAAARKG	HKCCGSHMA	AAAGAGANTT	YCMKAAARAC	CCGCGCHCCC	900
NAAAYACCC	MAAAWTTCH	AAASMSCNG	YCCGCC			936

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

MNNKNNNNY	ATMAYTCWY	YCTSCACCCG	GGNNKCNATT	GGGCGCRMAN	KCTTGTMAAS	60
AGATCTMNA	YTCGGCACAG	ASSGCGACAG	AGCGCGGGCG	CTATYCNKCG	GYTCTTCATG	120
CTCAACACCG	TCTTGGGGW	GRATAATGGC	NCGCGCCCGG	CGCGACACG	YTCATYTGCT	180
TGGCCACCCG	CATATNTCAA	CAAGGTGATA	AAASCAAAAC	CGCGCCGCTY	GGCTTTGGGC	240

SCGGRAASCU	GTGCCAACCC	EAAACNCKTT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TGKTCCTCT	GGGCTATGGT	GGGCCACAAA	CCTGTYGCGG	WGGGTCTGGC	CCTGGGGYCAC	360
GGYCRGCTTT	TATNTNTCK	YGTACACNCT	TGGGTTCAC	CAACCCACTT	CACNAATTC	420
TTTGGGGKTG	GGGSSGGCCG	YTGNKCCGK	TAATAATCGS	NTGKTCGGCC	MYCACCGGWA	480
GCATAGCTG	GGGGGCGCTG	GCAAAATTTC	AAAATCATYT	CCTTCTGTRAC	CCCCACAMEC	540
CTNSAAATCG	GRATCAAAC	CCCNKGGCTT	NTGCTGCTCN	GTCCGCAATY	TGGTTTCTAT	600
RKTNCCYAA	TSCAATTGGG	TTYCCTTTC	YGGTTCCAA	TTNACAAAG	GGTTTTCMT	660
ACCAAAACCC	NTGGSCNNA	CMNAAAACN	SAAAAAGGG	KCTTTAAAC	CCCCCCTAT	720
TCAWYCGGTN	CMNMCNCCG	NGKAAGGKH	GAAATTTKRA	CCCAANCCMT	ARSTTSGNAK	780
AAACCCYTCG	GGGTSMCAAA	MENTWTTSC	CTTCGGMCTT	YCCAAATMSA	ARATYTTCKE	840
KRMIAAAAC	YGNCCGCSAA	ANATTTTGT	MAACCGGKMA	YTTTTCMCC	WTTTTCCTCC	900
CCMNCSMSG	GTNCCCTTY	TYATTTCYM	MCNNNGACN	CCCNMTTYYT	TWTTCKWCH	960
MMARGSHYT	RGMMGNCCG	CCNCCCNAS	MTCCNCAAK	NTTTTACIN	NNKCKKCCC	1020
CCCNMKNKC	CCCNMCMTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:332:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(12) SEQUENCE DESCRIPTION: SEQ ID NO:332:

NMSGSGMKK	ATAMATCMT	CTSYACCCNO	GNTOMATTG	GGCCGMATC	TGTMASAG	60
ATCTGAAAY	CGGCAAAAK	ACGCMAYGT	AACTGTATY	CGGTGACATA	TGTTCCGCG	120
TCAACGCGA	AGCCGCTCA	CCGCTCCCT	GGGGCGCCAC	CCCATGGGT	RATGCAACT	180
CGCGCGGAC	GGYCAAAAG	GTCTTTRAG	CGCTAAAGT	CAMCAATTC	TGAGTYMCH	240
CACCTTNTT	TGGCGCGCC	RAWTCTTAC	CGGCAATTC	GGAATCGGR	AATTGGGCH	300
YCGGCTGGG	CAATAGRTN	TGGGCAAGC	CGGRTCTC	NTGGCGGRA	ATTCCGKAT	360
TGCTTAAAG	GTGTRACCT	TTTCCGGTT	CGGTAATTC	YTYCTGGGC	GGCTTCGGC	420
CGNAGCASY	CTCTACGGY	CMCAAGGCA	TACCTTGGC	TTTAAACCA	CGGRTAAAY	480
TGTAACGAC	YTCAGSSGT	CTGRANTTK	TNCTGTGAA	AAHMCCACN	AACCGGNTT	540
RATCTGCTC	MTCAACMTT	SCCGGCTTC	CGCGTTTTC	AACTTATC	CHTYCAAAAG	600
STTANTTTC	CCAAARAAT	CGYTTGCCA	CCTTGGCGG	GGCTGOTTM	CGMCTCTTR	660
AMATCCNCC	CGGGSAAAN	AMTTSAGNT	SGSCGCTTC	CCGNAATAT	YCTTGGNCT	720
GNAAATGSS	GGATTCGCT	GGNAYCCGG	CGWTGGGGK	TNCCCAATTG	GWACAATTYC	780
SKCCCTTCCA	AACCGGGNC	CGGCGGGTG	GGCCNTTTT	CCTMYNNAAA	AAGKCTTTN	840
NYTTTTCG	CMRAANTTA	CGSKNKNTT	GGNCCNACY	YTYCAANTTC	CANACCTTTA	900
AASAAANCY	YKTYTCCGC	TTTTCGSGS	SANCCGCGC	NMSKKKCGG	AAAAAAGNK	960
TGTCGTTAN	CMNKTKT	TNTYCCGCC	NMNNMSMCT	NCKKCNKRY	NMNNMNCCT	1020
MYKCKNNNN	SNNNNKNCH	GNCSGKNYM	GNNNCMNYE	NGNKNMCC	MSG	1073

(2) INFORMATION FOR SEQ ID NO:333:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1041 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(21) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GNSHGNHNTN	TMCAVCHWCT	SCACSGGGTC	TATTGGGGCC	GCAATYTNST	CKASAGATCT	60
GGATYTCGGC	AMHANAARTG	TCTTCCTCAA	TTCGAGKNTG	GTCTCTCAAY	GGGCGAGGCC	120
GNAGACCACRA	CCCTGNTGCA	CCCAAAANAC	CAACAGCWTG	AAATWTCAG	GCCGAGGSCC	180
TRTCAATYCC	CRASCAKTA	ACCGTKTCCW	TCAAGGTGTC	CRAACGAGGC	ACCCGAGYTCA	240
CGCGCCGGCA	ANTCCCGCTG	CGCGCCGGTN	TCAAGCGTAT	TYCTGACCTT	RWTCTGTBGG	300
TGGYCAMCHT	GGTGAAGGCG	CWMCSCGMA	AGRACTGGAG	GGCRAATTCG	CAGGAMCCNA	360
GRAACCCNAG	GAACCCCGCG	TAKAANCCGG	CRAAACCRAG	GGGUYTGGCN	ATTCCNATTA	420
NAMSGGTTTG	CRACNTGGCC	RAACCGITTY	CTTGGTCGGC	CTGGGCAACC	CTGGACCAAT	480
TACCCCKTNC	CGGNNMCNAC	CTCGGGTTCG	TGKYCCCAAT	NTGGYCCCGC	GNRANTNGCC	540
CNAATTCODG	GGCNCNANC	TTCGGGCGCN	AATTCCCTTG	GTTAATCACC	GGCGNCCCT	600
CGTTTTCGGC	AACCCCNCTY	CTTMTTAA	CATTCCGGCC	CAATGGGNC	NTGGGAAAT	660
TCNTVCGGT	GGGGCGGGR	AMMYTCTCT	YCCNAAAN	CTTAMYCCAN	TTCGSENTCC	720
CGGKCAJAS	NGGGCGGMA	AAGGGCCCCC	CGGNTSCCK	GGGGKGGCCC	CVGGKTTCAA	780
AANTTTCGGG	GXTSTMCGG	NYTSCCCCC	CGGCAAGRA	CGGNGTTTT	TTTTTGAACC	840
KCMANTSSA	AMCGCCGSC	CCNAAAGGS	GGCTHAANGS	RAYTNKSCC	CHNAAAGSGG	900
CGGCKARTY	GGKTTCHNC	CNCGSGKGT	CGMTSTTMM	MRCCCTTGN	GNKTTTTTAN	960
MGSCCTTNC	CACCCGCVCK	GGGKCMMA	GAATMYNWC	CNGGGGNBAN	RSCCGCGCN	1020
GGGKGGGSK	MGAGYSCCT	CTKCGGNCN	YHNTTCCCC	C		1061

(2) INFORMATION FOR SEQ ID NO:334:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Genomic DNA

(21) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GNNNNHKN	ATMCAYWY	UTSCACCSGG	GNTCNATTGC	GGCGGCANKY	TNTHAASAG	60
ATCTMGAAT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTCCANAG	CTGTCAACAC	120
GTGTGGCGSG	JTGSTRASCA	CMCATTCGGR	AACACCAAA	CGGTGGGGGG	GYCACGGCCG	180
TGGCTGTCAA	AACTCTCCAG	GGCAGCTYCA	AACAAYWYCT	CCTGCAACSC	ARSCCGTTTC	240
GGGGCGGAT	CTGSKYCAS	YTCGGKTCG	GGTGGGCCAA	GGTACTGGGC	CHYGRANACC	300
GCTTCGGGGA	ACCNAACTTA	AATGTTCGCG	AATTTGCTT	CGCGTSCCC	TTRATHAATT	360
TGTTAAACCA	CGCAAACTTY	CGGCGKTCG	CTGCTGCCRA	WTCCGRWTCC	RATNYCGGCA	420
TGGCTTNC	KYCTCKYKSC	GTMCACAAAT	CTTGGTATCC	TATATTGTCC	CTAAATGCCAA	480
ATCTKGGGCT	TGCATNTGCT	GGCTTTCAAA	TTWAMANCAG	NGGTTTCTTY	CTTCNAAAC	540
CGSTTGGGCC	CAACCCNAAA	AATGATNATA	ATAATGGTGC	TNTCAAAACC	CGCNCCTATY	600
GNATCGSGCC	AMMCCCGRG	GGTANKRGG	GNAATTCIMM	AACCCCAAGC	CTAASHTTTC	660
SGANAACTY	NCNCGGTYCA	CGAAACAN	NTTNTGCHY	SGNTCCGGM	YCATGGCTTN	720
CMAAARCCCN	AATACCTHYG	GGYCCATATA	AMMMSGGYC	SAMCCGGA	WTTTTTTC	780
KYNAAACGNA	AAKCTTTT	CNAAGCCBAN	WNTYCTTNCC	RCKRMANTUG	CNSGGARTKT	840
SSGCTTNC	ATGKYCCMAA	AGWGGGRANA	CCARCCGCAA	TTCCTNNNTN	KNKCCCHST	900
TRNAAAGGG	GIGTYNCMAA	AASCHGNC	NCNCTCCCAA	AACANCCCCN	AAAGARQTCN	960
NAANASKYSN	NNNSCCCCC	CCMMN				986

(2) INFORMATION FOR SEQ ID NO:335:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

((ii) MOLECULE TYPE: Genomic DNA

((xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NNNGGGNKN	ATMMAYCWT	GATYYACCSN	GGMMNMAITG	CGGCCRMAWT	CTNQTMAASA	60
GATCTMGAA	YTCGGCAAG	AGYATKCTCG	GGGGCCAGAT	TTNTGGCCCG	CAACCGCCGC	120
ACTTTGCAY	TCAACAKTCC	GGGTGCCCCA	AAAAANTCWT	ACCCCGCATC	TYCKTGCAAM	180
ASYTGGCCCC	RATTRAACAC	CGGGCCGGCC	CGGTGCCCCA	GGTATTYCAS	CAGYTCAAAY	240
YCTTTKTAG	TAAATCCAG	CGGGCCGGCC	CNCAGCCGGG	CGGTKTAGGT	GCCTYCTCA	300
ATMACCAGCY	CGCCGAGG	CACCTGCCCC	AAATYCTCTT	GGTTCAGCA	AATTYCGGCS	360
CGGGCCAAAC	ACCAACCGCA	TYCTGGCCTC	AATYTCACCG	CGCCGGGTCT	TAAAMMAAMA	420
GRATCTCTC	MANCCGCCAN	TCAGCGSYNA	CNCGMACAGC	CGCCCTTCTT	CAHACCCUCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACTCA	ACAGCGCGNC	AGGCTCTCCG	CGGANSAAAG	540
GTCTTACSC	NNYAAANAAA	MAAGTCTCTT	TTTCCCTCTC	CASAAASAAA	AANCCCCGCG	600
CGGGCCCTCN	NMMGGCTTC	GGGMAANAAA	AARCNCCGNN	GGACGNCATC	CGAAAMCTCC	660
CAAGTCNCT	TWANAACYCH	NNAACCCGCC	ANTTTTGGGA	AAGGNTCCCG	NTTMYCGCCG	720
TTTTTASGKS	GGGMYCTCT	TAAAAAAATT	CCCCAAAAG	CGCCGGGAAG	GGTCMACTG	780
GGNAATTC	CAACCMWOK	TTNTTNGGT	TMCGGGGORA	AATTYCTCTC	CCYNNNGGG	840
CGGSHMNAT	TAAGGMSMT	TTTMAAATM	NSGKKTSAAM	YNNCCMNNN	NNNMSMAHKK	900
TNACGCCCN	CCTCGGGKCT	GSCYNGCCG	CNAGNGRAS	MCCNMAKAA	AYASGKTTHK	960
CGGAANNNN	AATKNNMSC	CGCGASCMN	NNNMAAATM	CNCKNCNNN	AAHNGHACN	1020
CCCNNSGNN	NRGAARMTY	YCCGCCGSKM	GGKNKAAAM	GKTCCTCCCN	AAAG	1074

((2) INFORMATION FOR SEQ ID NO:336:

((i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

((ii) MOLECULE TYPE: Genomic DNA

((xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NGNNGNNNT	MTACATCWT	CTGACCCCGG	GNTCNANTGC	GGCCGCAWKY	TTGTGASAG	60
ATCTGAAAT	CGGCAGAGG	ACNCTCCGCA	CGCCGCCGCA	NACTCTGGCG	TGNTTACCCG	120
ATTGNGCCX	TCACCGCCCG	AYTANCCAK	TNCACTGGGG	TGCCCTYCGG	CTTGGCCGCG	180
GGCTTCAGG	CKCTGCTCT	RAAGGCTGSG	CGCACCGCAT	TGGGTTTTCT	RAAGCTCTGG	240
AAATGCGCA	CGGCTCTGGC	TCATGGGNTC	TACGCCAACG	CNCGCCCCAA	CACTTTCTTA	300
AATCGGKCC	NTCTTGAGCS	CTTTGAATCC	CGCGGSAAGA	ACTGTTCTGC	CNCGATCTGC	360
TGCAACTTXX	TCMAAATCCC	GCANAKTGTT	TCNTAMGYCC	CNCGGGAAGG	NGAACCTACT	420
TTGNGGWAG	TCGCGNCCCG	CGGCTTATCA	CTCTGTATCA	ACGGGGAACCT	GGYKNNNTTG	480
GGGAAAAAG	RRCTCTGAAT	MTYGGTCCCG	CCTCGCGKNC	CGCGCCCTGK	GYCGCNAATG	540
GAGGCGMAG	GTTTAAGGCC	MTTYCNYCCR	GGCGGTTGSA	SGKMTTYCGG	MCGANKAMNN	600
AACTCGGYCC	TCRNGGCGCC	ATSTSCCGGG	CKSTTAKAGA	AMACTYCKK	WCGGNTTYSC	660
SAAAGNTKCS	CGGNTTTTTT	SCGNGMAGNN	YCTGATTTSA	GGGGGYKYCC	CGCGGGCTTC	720
CGAANNKWKY	CTYAGGCGGG	CNYGAGCCSC	CGMNATNAG	AGNAAGGKTT	RYGSTEEMCC	780
TYNKGAGG	WCCNCGWSAK	ANAACNNKCT	TGCGCCNTMS	AGHKTNGKRT	YCCNKSTTTC	840
TAGAGGAGG	TATKMKGCCG	GKTSAGANMM	GAGWNGGCGC	KYCCCSNKRT	TCNTNGWAAA	900

TATKAGMGG	TECGGAGMK	CCGCTTTTKT	TKTQANAAMN	MSMKKHKKTG	GGMGYTCTSC	560
GGGNTTCTTA	GAGTAKTGGG	CSGSMWAGAC	WCGMCMGNG	AGNKTNTNTS	YANTGACGGY	1020
MNNKTKMNT	MSCSCGGGNA	GGAGNGCCCG	CSANGMSTGY	NKGNNMSSNG	ARAKGATGGG	1080
GGCNCMGNN	MGMGAMNGA	SAUNGMGMR	GGGGGKTGKC	TCKSCCCGNS	CSANGRAGAA	1140
GKTCNGSCCG	CGMGKGYKKT	KTKTKRKTGG	YSTCMEMMN	NAGAAAAAGG	AGCGCC	1196

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
 (B) TYPE: nucleic acid
 (C) STANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CCATCTGATC	GTTCGCRACC	AGCATGCGAG	TGGGAACGAT	GGCTCTATTC	AGCATTTGCA	40
TGGTTTGTGT	AAAAGCGGAC	ATGGCACTCC	AGTCCCTTTC	CGGTTCCGGT	ATCGGCTGAA	120
TTTGATTGCG	AAGTAGATAT	TTATGCCAGC	CAGCCGAGAC	CAGACGCGCC	GAGACAGAAC	140
TTAATGCGCC	CGCTAACACG	GGGATTTGGT	GGTGACCCAA	TGCGACCCGA	TGCTCCGCGC	180
CCAGTGGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGCTCAGAGA	300
CATCAAGAAA	TAACGCGGGA	ACATTATGTC	AGGCACTTTC	CACAGCAATG	GCATCTCTGT	360
CATCCAGGCG	ATAGTTTAATG	ATCAGGCGAC	TGACCGGTTG	CGCGAGAGA	TTGTCCACCG	420
CGGCTTTTCA	GGCTTCGACG	CGCTCTGGTT	GTACCATCGA	CACGACCCAG	CTGGGACCGA	480
GTGATCGCGC	CGCGAGATTG	ATCGCGCGCA	CAATTTGCGA	CGCGCGCTTC	AGGGCCAGAC	540
TGGAGGTGGC	AACGCGAATC	AGCAACGACT	GTTTGCGCGC	CAGTTGTTGT	GGCAGCGGCT	600
TGGGAACGTA	ATTGAGCTCC	GGCATGCGCG	CTTCGACTTT	TTCCGCGGTT	TTGCGAGAAA	660
GGTGGCTGGC	CTGGTTTACC	ACGCGGGAAA	CGGTCTGATA	AGAGACACCG	CAATCATCTG	720
CGACATGTTA	TAACGTTACT	GGTTTCACAT	TGCGACCTTT	GAATTGACTC	TGTTGCGCGC	780
GGTATGATCG	CATACCGCGA	AAGGTTTTGC	GGCATTCGAT	GGTGTCCGGG	ATCTCGACGC	840
TGCTGCTTAT	CGACCTGCTG	CATTAGGAAG	CAGCGCGATA	GTAGGTTGAG	GGCTTTGACG	900
ACCGCGCGCG	CAAGGAATGG	TGCATGGAAG	AGAGTACGCG	CGACAGCTTC	CGCGCGACGC	960
GGGCTTGCCA	TGATACCCAC	GGCGAAACAA	CGGCTCATGA	CGCGAGAGTG	CGCGGCGCGA	1020
TCTTCCGCAAT	CGGTGATGTC	GGCGATATAG	CGCGCCAGCA	CGGCACTGTT	GGCGGCGGTG	1080
ATCGCGGCGA	CGATCGGTTC	GGCTTAGAGG	ATCGAGATGT	CGATCCCGCG	GAATTAATAC	1140
GACTGACATAT	AGGGGAATTC	TGACCGGATA	ACAACTCCCG	TTTAGAAAAA	ATTTTGTTTA	1200
ACTTTAGAAA	GGAGATATAC	ATATGCGGCA	TCATCATCAT	CATCAGCTGA	TGCGACATGAT	1260
CGGACACAGC	CGACATCTCT	GGGAACAGGC	GGCGGCGGAG	GGGCTGACGT	GGGCGCGGGA	1320
TAGCGTCGAT	GACATCCGCG	TGCGTCCGGT	CATTGACGAG	GACATGGCGG	TGACACAGCG	1380
CGCGAAGATG	ACCTACCGCA	TCAAGCTCGA	AGTGTCTGTT	AAGATGAGCG	CGCGCGACCC	1440
GAGGCGCTCG	AAACACCGGA	CGGTTTCCGC	TGAAACCGGG	CGCGGCGCGC	GTACTGTGCG	1500
CGGACCTCTC	CGCTCGTGGC	CGGTGACGTT	GGCGGAGACG	GTTAGGACGC	CTCTCTACCC	1560
GCTGTTTAAK	CTGTGGGGTC	GGGCTTTTCA	CGAGAGGTAT	CGGAACGTCA	CGATCAGCGC	1620
TCAAGGCGAC	GGTTCTGGTG	CGCGGATCGC	CGAGCGCGCT	CGCGGAGACG	TCAACATTCG	1680
GGCGCTGACG	GGCTATCTGT	CGGAAGGTGA	TATGCGCGCG	CACAGGGGCG	TGATGAACAT	1740
CGCGCTGACG	ATCTCCGCTC	AGCAGGTCAA	CTACAAAGCT	CGCGAGTGA	CGGAGCAGCT	1800
CAGGCTGAGC	GGAAAGATCC	TGGCGGCGAT	GTACACAGGG	ACCATCAAAA	CTCTGGACGA	1860
CGCGCAGATC	GTCGGGCTCA	ACCGCGGCGT	GAACCTTGCG	GGCACCGCGG	TAGTTCCGCT	1920
GACCGGCTCG	GACGGGTGCG	GTGACAGCTT	CTTTCTTACC	CAGTACCTGT	CGAAGCAAGA	1980
TCCCGAGGCG	TGGGCGAAGT	CGCGCGGCTT	CGGCGACGAC	GTGCACTTCC	CGCGGCTGCC	2040
GGTGGCGCTG	GGTGAGAACG	CGAACGCGCG	CATGTTGACG	GGTTCGCGCG	AGACACCGCG	2100
CTGGGTGGCG	TATATCGGGA	TGAGGTTCTT	CGACACGCGG	AGTCACAGGG	GACTCGGEGA	2160
GGCGCAAGTA	GGGAATAGCT	CTGGCAATTT	CTGTCTGCGT	GACGCGCAAA	GCATTCAGGC	2220


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CCCCGGCGCT GGCTTCGCAT CGAAAACCCC GCGGAACGAG GCGATTTTGA TGATCGACGG 2280
CCCCCGCCCG GACCGCTACG CAGATCATCA CTACGAGTAC GGCATCGTCA ACACCGGCGA 2340
AAAGGACGCC GCGACCGCGC AGACCTTGCA GGCATTTCTG CACTCGGCGA TCACCGACGG 2400
CAACAAGGCC TCGTTCTCTG ACCAGGTTCA TTCTGAGCGG CTGCGCGCGG CCGTGGTGAA 2460
GTTGTCGTAC GCGTTGATCG CAGCGATTCG CAGCGCTGAG ATGAAGACCG ATGCGCGTAC 2520
CTTGCGCGAG GAGCGAGGTA ATTTGAGCGG GATCTCGGGC GACCTGAAAA CCGAGATCGA 2580
CCAGGTGGAG TCGACCGCAG GTTCTGTGCA GGGCCAGTGG CCGCGCGCGG CCGGGACGGC 2640
CGCGCAGGCG GCGGTGGTGC GCTTCCAAGA AGCAGCCAAAT AAGCAGAAGC AGGAATCGA 2700
CGAGATCTCG ACGAATATTC GTCAAGCGCGG CGTCCAAATC TCGAGGGCGG ACGAGGAGCA 2760
CGAGCAGCGG CTGTCTCTGC AAATGGGCTT TGGATTTCAG TTGCGGCTGG CTGCTGGCTG 2820
GGTGGAGTCT GACGCGCGCG ACTTGGACTA CGGTTCAAGC CTCTTCAGCA AAACACCGGG 2880
GGACCGCGCA TTTCGCGGAC AGCGCGCGCG GGTGGCCAAT GACACCGGTA TCGTGCTCGG 2940
CGCGCTAGAG CAAAAGCTTT ACGCCAGCGC CGAAGCCACC GACTCCAGG CCGCGGCGCG 3000
GTTGGGCTCG GACATGGGTG ATTCTATATG GCGCTACCGG GGCACCGCGA TCACACGAGA 3060
AACCGTCTCG CTYAGCGGCA ACGGGGTGTC TGGAGCGCGG TCGTATTAC AAGTCAAGTT 3120
CAGCGATCTG AGTAAAGCGA ACGCGCGGAT CTGGACGGGC GTAATCGGCT CCGCCGCGGC 3180
GAACGCGCGG GACCGCGGCG CCGCTCAAGC CTGGTTTGTG GTATGGCTCG GACCGCGGAA 3240
CAACCGGCTG GACAGGCGCG CGGCCAAGCG GGTGGCGGAA TCGATCGGGC GTTGGTCTGC 3300
CGCGCGCGCG GCGCGCGGCG GGGAGGTGCG TCTTACCGCG ACGACACCGA CACCGCGAGG 3360
GACCTTAGCG GCTTAGAAT TCTGCAGATA TCGATCACAG TGGCGCGCGC TCGAGCACCA 3420
CGACCGCGAC CACTGAGGTC CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AATTGGCTGC 3480
TGGACCGGCT GAGCAATAC TAGCATAACG CTTGGGCGCG TCTAAACCGG TCTTGAAGGG 3540
TTTTTGTCTG AAAGGAGGAA CTATATCGGG AT 3572

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
1             5             10             15
Asp Gly Xaa Arg
20

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
1             5             10

```

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Thr Xaa Glu Glu Xaa Glu Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
 1 5 10 15
 Xaa Lys

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CTAGTTAGTA CTCAGTCCCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGTGCAGCA ATTCACCTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CATATGGGCT	ATCATCATCA	TCATCACCTG	ATCGACATCA	TGGGGACCCG	CCCCACATCC	60
TGGGAACAGG	CGGCGCGCGG	GGCGGTCGAG	CGGCGCGCGG	ATAGCGTGGG	TCACATCCGC	120
GTGCGCTCGG	TCATTGAGCA	GGACATGGCC	GTGGACAGCG	CCGCGCAAGAT	CACCTACCCG	180
ATCAAGCTTC	AAGTGTGCTT	CAAGATGAGG	CGGCGCGCAAC	CGAGGGGGCTC	GAAACACCCG	240
AGCGGTTCCG	CTGAACAGCG	CGCGCGCGCC	GGTACTGTGG	CGACTACCCC	CGCGTCTCTG	300
CGCGTGAAGT	TGGCGGAGAC	CGGTAGCAGC	CTGCTCTACC	CGCTCTTCAA	CGCTGTGGGT	360
CGCGGCTTTC	ACGAGAGGTA	TCCGAACCTC	ACGATCACCG	CTCAAGGGCAC	CGGTTCTGGT	420
CGCGGAGTGC	CGCAGGCTCC	CGCCGGGAGC	GTCAACATTC	GGGCGCTCGG	CGCTATCTCG	480
TCCGAAGGTC	ATATGGCTGC	GCACAAGGGG	CTGATGAACA	TGGCGGTAGC	CATCTCGGCT	540
CAGCAGGTCA	ACTACACACT	GCCCGGAGTC	AGCGAGCACC	TGAAGCTGAA	CGGAAAAGTC	600
GTGGCGCGCA	TGTACGAGGG	CACCATCAAA	ACCTGGGAGC	ACCGCCAGAT	CGCTGCCTTC	660
AACCCCGGCG	TGAACCTTGC	CGGCACCGCG	GTAGTTCCCG	TGCAGCGGTC	CGACGGGTCC	720
GGTGACACTC	TCTTBTTCAC	CCAGTACCTC	TCCAGGCAAG	ATCCCGAGGG	CTGGGGCAAG	780
TGGCCCGGCT	TGGGCAGCAC	CGTCGACTTC	CGGCGCGGTC	CGGCTCGGCT	CGGTGAGAAC	840
GGCAACGGCG	GCATGGGTAC	CGGTTCCGCG	GAGACACCGG	GCTGCTTGGC	CTATATCGGC	900
ATCAGCTTCC	TGACCGAGGC	CAGTCAACCG	GGACTCGGCG	AGGCCCAACT	AGCCAAATAGC	960
TCTGGCAATT	TCTTGTGTGC	CGAGCGCGAA	AGCATTCAGG	CCGCGCGCGC	TGGCTTCGCA	1020
TGGAAGACCC	CGGCGAACCA	CGCGATTTCG	ATGATCGAGC	GGCGCGCGCC	GGACGGCTAC	1080
CGATATCATC	ACTACAGTGA	CGGCATCTCT	AACACCGCGC	AAAAGGACGC	CGCCACCGCG	1140
CAGACCTTCC	AGGCATTTCT	GCAGTGGAGG	ATCAGCGAGC	GCAACAAGGC	CTCGTTCTCT	1200
GACCAAGTTC	ATTTCGAGGC	GCTGCGCGCC	CGGCTGGTGA	AGTTGTCTGA	CGCGTTGACT	1260
CGACACATTC	TCAGCGCTGA	GATGAAGACC	GATGCGCGTA	CGCTCGCGCA	GGAGGCAGGT	1320

180					185					190					
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
195						200						205			
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
210						215						220			
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
225					230					235				240	
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
					245					250				255	
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
					260					265				270	
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys
					275					280				285	
Ala	Gln	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp
					290					295				300	
Gln	Ala	Ser	Gln	Arg	Gly	Leu	Gly	Gln	Ala	Gln	Leu	Gly	Asn	Ser	Ser
305					310					315				320	
Gly	Asn	Phe	Leu	Leu	Pro	Asp	Ala	Gln	Ser	Ile	Gln	Ala	Ala	Ala	Ala
					325					330				335	
Gly	Phe	Ala	Ser	Lys	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Ser	Met	Ile	Asp
					340					345				350	
Gly	Pro	Ala	Pro	Asp	Gly	Tyr	Pro	Ile	Ile	Asn	Tyr	Glu	Tyr	Ala	Ile
					355					360				365	
Val	Asn	Asn	Arg	Gln	Lys	Asp	Ala	Ala	Thr	Ala	Gln	Thr	Leu	Gln	Ala
					370					375				380	
Phe	Leu	His	Trp	Ala	Ile	Thr	Asp	Gly	Asn	Lys	Ala	Ser	Phe	Leu	Asp
385					390					395				400	
Gln	Val	His	Phe	Gln	Pro	Leu	Pro	Pro	Ala	Val	Val	Lys	Leu	Ser	Asp
					405					410				415	
Ala	Leu	Ile	Ala	Thr	Ile	Ser	Ser	Ala	Glu	Met	Lys	Thr	Asp	Ala	Ala
					420					425				430	
Thr	Leu	Ala	Gln	Glu	Ala	Gly	Asn	Phe	Glu	Arg	Ile	Ser	Gly	Asp	Leu
					435					440				445	
Lys	Thr	Gln	Ile	Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly
					450					455				460	
Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg
					465					470				475	
Phe	Gln	Gln	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu	Ile	Ser
					480					485				490	
Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu	Gln
					500					505				510	
Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe	Val	Pro	Thr	Thr	Ala
					515					520				525	
Ala	Ser	Pro	Pro	Ser	Thr	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro
					530					535				540	
Val	Ala	Pro	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro
					545					550				555	
Gly	Asp	Pro	Asn	Ala	Ala	Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro
					560					565				570	
Pro	Pro	Val	Ile	Ala	Pro	Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn
					580					585				590	
Pro	Val	Gly	Gly	Phe	Ser	Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser
					595					600				605	
Asp	Ala	Ala	His	Phe	Asp	Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr
					610					615				620	

Gly	Asp	Pro	Pro	Phe	Pro	Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr
625				630						635				640	
Arg	Ile	Val	Leu	Gly	Arg	Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu
			645					650						655	
Ala	Thr	Asp	Ser	Lys	Ala	Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu
			660					665						670	
Phe	Tyr	Met	Pro	Tyr	Pro	Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser
		675					680					685			
Leu	Asp	Ala	Asn	Gly	Val	Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys
	690			695							700				
Phe	Ser	Asp	Pro	Ser	Lys	Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile
	705			710						715				720	
Gly	Ser	Pro	Ala	Ala	Asn	Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp
			725					730						735	
Phe	Val	Val	Trp	Leu	Gly	Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala
		740					745						750		
Ala	Lys	Ala	Leu	Ala	Glu	Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro
		755				760					765				
Ala	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala
	770			775						780					
Gly	Glu	Val	Ala	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu
	785			790						795				800	
Pro	Ala														

(2) INFORMATION FOR SEQ ID NO:347:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Other

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGATCCAAAC CACGAGCCGG TTCCCTGAA ACCG

34

(2) INFORMATION FOR SEQ ID NO:348:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: Other

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CGCTGCGAAT TCACCTCCGG AGGAAATGCT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:349:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(14) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

CATATGGGGC ATCATCATCA TATATCAAGG TCCAAACCA CAGACCGGTT C GCTTGAAACG 60
GGCGCGGGCG CCGGTACTGT GCGCACTACC GCGCGGTGCT GCGCGGTGAC GTTGGCGGAG 120
ACCGGTAGCA CGCTGCTCTA GCGCTGTTTC AACCTGTGGG GTCCGGCGCTT TCACGAGAGG 180
TATCCGAGCG TCACGATCAC CGCTCAGGGC ACCGTTCTGT GTCCGGGGAT GCGCAGGGCC 240
GCGCGCGGGA CGGTCAACAT TGGGGGCTCC GACGCTTATC TGTGGGAAGG TGATATGGCC 300
GCGCACAGGG GCGTATGAA CATCGCGCTA GCGATGTCCG CTCAGCAGGT CAACTACAGC 360
GTGCGCGGAG TGAGCGAGCA CCGCAAGCTG AACGGAAGG TCGTGGCGGG CATGTACCAG 420
GCGACCATCA AAAGCTTGGA CGACCGCGAG ATCGCTGCGC TCAACCCCGG CGTGAAGCTG 480
GCGCGCAGCG CGGTAGTTCC GGTGCACCCG TCCAGCGGTT CCGGTGACAC CTCTTTGTTT 540
ACCCAGTACC TGTCCAGCA AGATCGCGAG GCGTGGGGCA AGTGGCGGCG GTTGGCGAGT 600
ACCGTCAACT TCGCGCGGCT GCGGGGTGCG GTGGGTGAGA ACCGCAACGG CGGCATGGTG 660
ACCGTTTTCG CGAGACACC GCGCTCGCTG GCTATATCG GATCAGCTTT CTTGACAGAG 720
GCGAGTCAAC GCGGACTCGG CGAGCGCCAA CTAGGCAATA GCTTGGGCAA TTCTTGTGTT 780
GCGGAGCGCG AAAGCATTC GCGCGCGCGG GCTGGCTTTC CATCGAAAG CCGCGCGAAC 840
CAGGCGATTT CAGTATCGA CCGCGCGGCT CCGGACGGCT ACCGATCAT CAGTACAGAG 900
TACGCTATCG TCACAGACCG GCAAAAGGAC GCGGCGACCG CGCAGACCTT GCAGGCATT 960
TTGGATTCGG CAGTACCGA CGGCAACAG GCGTGGTTCG TCGACAGGTT TCATTTTCAG 1020
GCGGCTCGCG CCGCGGTTGT GAATTTGTGT GAGCGTTTGA TCGGACAGAT TTCTTCGGA 1080
GCTGCACTG CGGAGGCTC AGTTCGAGGT TCTGGGAGGA GCGTGGCGAC AACGCGCGCC 1140
TGGCGCGGCT CGAGCTCTGC AGTGGCAGCT GCACTCGGGA CAGCTGTTGC CCGCGCACCA 1200
GCGCGCGCGG TCAACAGCGT GAATGCTCAG CCGGCGGATG TCAACCGACG ACCTTCGCGG 1260
GCGGAGCGGA AGCGACTCGC GCGAGCTTTC ATTGCGCGAA AGCGCGCGGA ACCTTCGCGG 1320
ATCGACAGCG CGGTTCAGGG ATTACAGCTTC GCGCTGCTCG GTGGCTGGGT GAGCTGTGAC 1380
GCGCGGACTT TCGACTACGG TCGACAGCTC CTCAGCAAAA CGACCGGAGA CCGCGCATTT 1440
GCGGAGACAG CCGCGCGGCT GCGCAATGAC ACCGATATCG TCGTCCGGCG CTTAGACCAA 1500
AAGCTTTAGC CGAGCGCGGA AGCAGCTGAC TCGAAGCGCG CCGCGCGGCT GCGCTCGGAC 1560
AGCGGTGAGT TCTATATGCC CTACCGCGGG ACCCGGATCA ACCAGGAAGC CGTCTCGCTC 1620
GACCGCAACG GCGTGTCTGG AAGCGCGTCC TATACCAAG TCAAGTTTAC CGATTCGAGT 1680
AAGCTGAACG CGCAGATCG GAGCGGCGTA ATCGGCTCGG CCGCGCGGAA CGCACCTGAC 1740
GCGCGCGCGC CTCAGCGCTG GTTCTGTGTA TCGCTCGGGA CCGCGCAACA TCGCGTGGAC 1800
AAGGCGCGCG CGAGCGGCT GCGCGAATCG ATCGGCTCTT TCGTCCGCGC CCGCGCGGCG 1860
CGCGCACCGG TCGCTGAGGA CGCGGCTCGG GCGCGCGGCG GCGCGGCGGA AGTGTCTCT 1920
ACCGCGAGCA CAGCGACACT CGAGCGGAGC TTACCGGCT GA

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(2) INFORMATION FOR SEQ ID NO:150:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(14) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1 5 10 15
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20 25 30
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35 40 45
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50 55 60
 Ile Thr Ala Glu Gly Thr Gly Ser Gly Ala Gly Ile Ala Glu Ala Ala
 65 70 75 80
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85 90 95
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 100 105 110
 Ala Glu Glu Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Cys
 115 120 125
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Glu Gly Thr Ile Lys Thr
 130 135 140
 Trp Asp Asp Pro Glu Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 145 150 155 160
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 165 170 175
 Phe Leu Phe Thr Glu Tyr Leu Ser Lys Glu Asp Pro Glu Gly Trp Gly
 180 185 190
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 195 200 205
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 210 215 220
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Glu Ala
 225 230 235 240
 Ser Glu Arg Gly Leu Gly Glu Ala Glu Leu Gly Asn Ser Ser Gly Asn
 245 250 255
 Phe Leu Leu Pro Asp Ala Glu Ser Ile Glu Ala Ala Ala Ala Gly Phe
 260 265 270
 Ala Ser Lys Thr Pro Ala Asn Glu Ala Ile Ser Met Ile Asp Gly Pro
 275 280 285
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 290 295 300
 Asn Arg Glu Lys Asp Ala Ala Thr Ala Glu Thr Leu Glu Ala Phe Leu
 305 310 315 320
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Glu Val
 325 330 335
 His Phe Glu Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 340 345 350
 Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 355 360 365
 Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 370 375 380
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 385 390 395 400
 Ala Ala Ala Asn Thr Pro Asn Ala Glu Pro Gly Asp Pro Asn Ala Ala
 405 410 415
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro
 420 425 430

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 435 440 445
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 450 455 460
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 465 470 475 480
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 485 490 495
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 500 505 510
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 515 520 525
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 530 535 540
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 545 550 555 560
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 565 570 575
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 580 585 590
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Gln
 595 600 605
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 610 615 620
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 625 630 635 640
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 645 650

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference 9532-023-228	IMPORTANT DECLARATION	Date of mailing (day/month/year) 22 JUNE 1999
International application No. PCT/US99/03265	International filing date (day/month/year) 17 FEBRUARY 1999	(Earliest) Priority Date (day/month/year) 18 FEBRUARY 1998
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant CORIXA CORPORATION		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
- a. ☐ scientific theories.
 - b. ☐ mathematical theories.
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☐ diagnostic methods practiced on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
- ☐ the description
 - ☐ the claims
 - ☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:
- ☒ it does not comply with the prescribed standard
 - ☐ it is not in the prescribed machine readable form
4. Further comments:

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Form PCT/ISA/303 (July 1992)*

Authorized official

MICHAEL WOODWARD

Telephone No. (703) 308-4078

DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT

International application No.

PCT/US99/03265

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(5): A61K 38/00; C07K 1/00; C07K 16/00; C12Q 1/68; C12P 19/34; C07H 21/02, 21/04
US Cl. 530/300, 350, 387.1; 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32.2⁺, 33